

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 14, 2005, 15:01:02 ; Search time 177 Seconds
(without alignments)
1886.303 Million cell updates/sec

Title: US-10-614-076-98

Perfect score: 3406

Sequence: 1 MNPNNRSEHTIKVPENSEL.....SFVSNKIIYDKIEFIPVOL 652

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3406	100.0	652	1	C3BB_BACTU
2	3212	94.3	659	1	C3BA_BACTO
3	2341.5	68.7	644	1	C3AA_BACTT
4	2341.5	68.7	652	2	Q9S6N9
5	2337.5	68.6	652	2	Q6PXN8
6	2319.5	68.1	652	2	Q643Z7
7	2152	63.2	649	1	C3CA_BACTK
8	1272.5	37.4	1144	2	Q8KZL7
9	1205.5	35.4	1157	1	C8AA_BACUK
10	1166.5	34.2	1159	1	C8BA_BACUK
11	1127.5	33.1	1157	1	C9CA_BACTO
12	1124.5	33.0	719	1	C1IB_BACTE
13	1122	32.9	1223	1	C1BB_BACTU
14	1122	32.9	1233	1	C1BC_BACTM
15	1121	32.9	1215	1	C1KA_BACTM
16	1119	32.9	1138	1	C7AA_BACTU
17	1118.5	32.8	719	2	Q9F0P8
18	1117	32.8	1138	1	C7AB_BACUK
19	1115.5	32.8	719	1	C1ID_BACTU
20	1112	32.6	1138	1	C7AB_BACUA
21	1100.5	32.3	719	1	C1IA_BACTK
22	1100.5	32.3	719	2	Q93N75
23	1100.5	32.3	719	2	Q6X181
24	1096.5	32.2	719	2	Q8K761
25	1094.5	32.1	719	2	O85796
26	1072.5	31.5	1228	1	C1BA_BACTK
27	1071.5	31.5	1228	2	Q93N75
28	1070.5	31.4	1228	2	Q93T75
29	1060	31.1	1160	1	C8CA_BACTP
30	1060	31.1	1160	2	Q6R2R6
31	1053	30.9	1231	2	Q8KNY2

32	1046.5	30.7	719	1	C1IC_BACTU	O87404	bacillus	th
33	1042	30.6	1231	1	C1BD_BACTZ	O92a25	bacillus	th
34	1041.5	30.6	1169	1	C9DA_BACTP	O6014	bacillus	th
35	1018	29.9	1154	2	Q6QAN9	O6qan9	bacillus	th
36	1013	29.7	849	2	Q6PYW8	O6pyw8	bacillus	th
37	1013	29.7	1227	1	C1BE_BACTU	O85805	bacillus	th
38	999.5	29.3	645	2	Q9S603	O85603	bacillus	th
39	995	29.2	1150	1	C9EA_BACTA	O92n19	bacillus	th
40	995	29.2	1150	2	Q71RP4	Q71rp4	bacillus	th
41	975	28.6	1163	1	CQAA_BACTP	Q9x597	bacillus	th
42	963.5	28.3	1144	2	Q45745	Q45745	bacillus	th
43	934.5	27.4	1189	1	C1CA_BACTE	O5518	bacillus	th
44	934.5	27.4	1189	2	Q6YNB8	P05nb8	bacillus	th
45	932.5	27.4	1189	2	Q9L877	O9l877	bacillus	th
46	909	26.7	793	2	Q6PYW7	Q6pyw7	bacillus	th
47	899.5	26.4	1155	1	C1AE_BACTK	P06578	bacillus	th
48	899.5	26.4	1155	2	Q7BE98	Q7be98	bacillus	th
49	899.5	26.4	1155	2	Q9F296	Q9f296	bacillus	th
50	898.5	26.4	1156	2	Q6GUA7	O6gua7	bacillus	th
51	898.5	26.4	1174	1	C1FA_BACTA	O03746	bacillus	th
52	897	26.3	1118	2	Q9AM63	Q9am63	bacillus	th
53	893.5	26.2	1177	2	Q6BIX3	Q6biX3	bacillus	th
54	891.5	26.2	1155	2	Q93T21	Q93t21	bacillus	th
55	888	26.1	1181	1	C1AE_BACTL	P56953	bacillus	th
56	886.5	26.0	1176	1	C1CB_BACTG	Q03748	bacillus	th
57	883.5	25.9	1179	1	C1AD_BACTA	O03744	bacillus	th
58	876	25.7	1176	2	Q7WZT9	Q7wzt9	bacillus	th
59	874	25.7	1180	2	Q9S5V8	Q9s5v8	bacillus	th
60	873.5	25.6	1171	2	O06894	O06894	bacillus	th
61	870	25.5	620	2	Q45720	Q45720	bacillus	th
62	870	25.5	1176	2	Q45736	O45736	bacillus	th
63	869.5	25.5	1171	1	C1EA_BACTX	O54758	bacillus	th
64	869.5	25.5	1171	2	Q71TM6	Q71tm6	bacillus	th
65	867.5	25.5	1177	2	Q45735	Q45735	bacillus	th
66	867.5	25.5	1177	2	Q8GLY5	Q8gly5	bacillus	th
67	867	25.5	1178	1	C1AC_BACTK	P05068	bacillus	th
68	867	25.5	1178	2	Q6XLN7	Q6xln7	bacillus	th
69	866.5	25.4	1166	1	C1GA_BACTU	O45746	bacillus	th
70	866	25.4	1176	1	C1AA_BACTK	P02965	bacillus	th
71	865.5	25.4	829	2	Q6BE06	Q6be06	bacillus	th
72	865	25.4	1176	2	Q9RC30	Q9rc30	bacillus	th
73	863	25.3	1178	2	Q9R826	Q9r826	bacillus	th
74	862	25.3	618	2	Q32306	O32306	bacillus	th
75	861.5	25.3	607	2	Q45721	O45721	bacillus	th
76	861.5	25.3	618	2	Q45737	O45737	bacillus	th
77	861.5	25.3	723	2	Q9S4B5	Q9s4b5	bacillus	th
78	861.5	25.3	1177	2	Q03743	Q03743	bacillus	th
79	861.5	25.3	1177	2	Q71JF1	Q71jf1	bacillus	th
80	861	25.3	1178	2	Q45768	Q45768	bacillus	th
81	859.5	25.2	1170	1	C1JB_BACTU	O45716	bacillus	th
82	854.5	25.1	1169	2	O8GH8	O8gh8	bacillus	th
83	850.5	25.0	1169	1	C1GB_BACTZ	Q92a26	bacillus	th
84	846	24.8	1169	2	C1FB_BACTM	Q66377	bacillus	th
85	845	24.8	1174	2	Q45749	O45749	bacillus	th
86	844	24.8	1167	1	C1JA_BACTU	O45738	bacillus	th
87	841	24.7	648	1	CJAA_BACTJ	O32307	bacillus	th
88	838.5	24.6	1165	1	C1DA_BACTA	P19415	bacillus	th
89	838	24.6	793	2	Q6PYW9	Q6pyw9	bacillus	th
90	835	24.5	1174	1	C1EB_BACTA	Q03745	bacillus	th
91	828	24.3	1160	2	C1DB_BACTU	O45747	bacillus	th
92	828	24.3	1160	2	Q93TF9	Q93tf9	bacillus	th
93	821	24.1	825	2	Q6BE09	O6be09	bacillus	th
94	816	24.0	1332	2	Q765X5	O765x5	paenibacill	
95	811.5	23.8	660	2	Q8ROU6	Q8roU6	bacillus	th
96	810.5	23.8	1118	2	Q9AM82	Q9am82	bacillus	th
97	807	23.7	1176	2	Q9S514	Q9s514	bacillus	th
98	805.5	23.6	1344	2	Q765X7	Q765x7	paenibacill	
99	797.5	23.4	782	2	Q6PYW6	O6pyw6	bacillus	th
100	796	23.4	911	1	C1AF_BACTU	P96315	bacillus	th
101	788	23.1	1155	1	C1HE_BACTM	O45718	bacillus	th
102	787.5	23.1	1172	1	C1HA_BACTU	Q45748	bacillus	th
103	783	23.0	1176	1	C1AG_BACTU	O9s515	bacillus	th
104	773.5	22.7	686	2	Q75Q05	Q75q05	bacillus	th

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105 748.5 22.0 1118 2 Q9AM81
106 745 21.9 1170 2 Q6Q7C6
107 718 21.1 682 1 C3BA_BACUH
108 700 20.6 381 2 Q45740
109 685 20.1 1280 2 Q8VUK9
110 679 19.9 1156 1 C9AA_BACTG
111 676.5 19.9 405 2 Q765X3
112 669.5 19.7 675 2 Q8KNV2
113 665.5 19.5 675 1 C9AA_BACTI
114 663.5 19.5 1236 2 Q939T3
115 656.5 19.3 1136 1 C4BA_BACTI
116 639 18.8 810 2 Q6SE03
117 637.5 18.7 1180 1 C4AA_BACTI
118 631.5 18.5 675 2 Q6BCH5
119 626.5 18.4 1109 1 CSAA_BACTF
120 625.5 18.4 674 1 C9AA_BACTU
121 623.5 18.3 1128 2 Q9FDC0
122 613.5 18.0 1254 2 Q8VUL0
123 604 17.7 666 2 Q8VM62
124 600.5 17.6 666 2 Q7X3F7
125 600 17.6 753 1 CKAA_BACUF
126 594.5 17.5 683 2 Q75VA2
127 573.5 16.8 650 2 Q8VNX2
128 567.5 16.7 688 2 Q8VNX1
129 535 15.7 675 1 CPAA_BACTU
130 534 15.7 826 1 C9AA_BACUH
131 520 15.3 618 1 CHAA_CLOBI
132 483 14.2 1155 2 Q9AM80
133 482 14.2 613 1 CGAA_CLOBI
134 472 13.9 1270 1 Q8VUL1
135 316 9.3 1257 1 C3AA_BACTU
136 301 8.2 297 2 Q45789
137 279.5 8.2 1245 1 CSBA_BACTU
138 277.5 8.1 1286 2 Q8KZM2
139 272.5 8.0 1167 1 CLAA_BACTU
140 262 7.7 633 1 C2AD_BACTU
141 255.5 7.5 196 2 Q6S554
142 251.5 7.4 633 2 Q6RPF60
143 248.5 7.3 633 2 Q9S6N5
144 247.5 7.3 193 2 Q6S553
145 247 7.3 633 2 Q8GH90
146 245.5 7.2 633 1 C2AA_BACTK
147 245.5 7.2 633 2 Q71SV7
148 245.5 7.2 633 2 Q8GHF3
149 245 7.2 633 1 C2AB_BACTK
150 242 7.1 633 2 Q7X2S7

ALIGNMENTS

RESULT 1
C3BB_BACTU
ID C3BB_BACTU STANDARD; PRT; 652 AA.
AC Q06117; Q45717;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Pesticidal crystal protein cry3Bb (insecticidal delta-endotoxin
DE CryIIIB(b)) (Crystalline entomocidal protoxin) (74 kDa crystal
DE protein).
GN Name:cry3Bb; Synonyms:cryIIIB(b), cryIIIB2;
OS Bacillus thuringiensis;
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EG4961;
RX MEDLINE=93119147; PubMed=1476436;
RA Donovan W.P., Rupar M.J., Slaney A.C., Malvar T., Gawron-Burke M.C.,
RA Johnson T.B.;
RT "Characterization of two genes encoding Bacillus thuringiensis
RT insecticidal crystal proteins toxic to Coleoptera species.";

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Q9AM81 bacillus th
Q6Q7C6 bacillus th
Q45740 bacillus th
Q8VUK9 bacillus th
Q939T3 bacillus th
Q765X3 paenibacill
Q8KNV2 bacillus th
Q939T3 bacillus th
Q939T3 bacillus th
Q6BE03 bacillus th
Q1480 bacillus th
Q6BCH5 bacillus th
Q9X682 bacillus th
Q87905 bacillus th
Q9FDC0 bacillus th
Q8VUL0 bacillus th
Q8VM62 bacillus th
Q7X3F7 bacillus th
Q32321 bacillus th
Q75VA2 bacillus th
Q8VNX2 bacillus th
Q8VNX1 bacillus th
Q87906 bacillus th
Q9S597 bacillus th
Q05102 clostridium
Q9AM80 bacillus th
Q45982 clostridium
Q8VUL1 bacillus th
Q45789 bacillus th
Q45712 bacillus th
P56956 bacillus th
Q9XMG3 bacillus th
Q6S554 bacillus th
Q6KF60 bacillus th
Q9S6N5 bacillus th
Q8GH90 bacillus th
P21253 bacillus th
Q71SV7 bacillus th
Q8GHF3 bacillus th
P21254 bacillus th
Q7X2S7 bacillus th

App. Environ. Microbiol. 58:3921-3927(1992).
[2]
SEQUENCE FROM N.A.
STRAIN=NRRL B-18655 / EG5144;
Donovan W.P., Rupar M.J., Slaney A.C.;
"Bacillus thuringiensis cryIIIC, (b) protein toxic to coleopteran
insects.";
Patent number US5378625, 03-JAN-1995.
-!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
epithelial cells of Coleoptera. Has moderate level of toxicity to
southern corn rootworm.
-!- SUBUNIT: Monomer.
-!- DEVELOPMENTAL STAGE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part of
the spore coat.
-!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
terminus.
-!- SIMILARITY: Belongs to the delta endotoxin family.

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EMBL; M89794; AAA22334.1; -;
EMBL; U31633; AAA74198.1; -;
PIR; I39811; I39811.
PDB; 1J16; X-ray; A=64-652.
InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin C.
InterPro; IPR005639; endotoxin N.
InterPro; IPR008979; Gal_bind_Like.
Pfam; PF03944; Endotoxin M; 1.
Pfam; PF03945; Endotoxin N; 1.
3D-structure; Sporulation; Toxin.
VARIANT 21 21 Q -> P (in strain EG5144).
VARIANT 97 97 N -> D (in strain EG5144).
VARIANT 289 289 I -> V (in strain EG5144).
VARIANT 352 352 F -> S (in strain EG5144).
VARIANT 417 419 VVL -> IYF (in strain EG5144).
VARIANT 451 451 S -> G (in strain EG5144).
VARIANT 590 590 L -> I (in strain EG5144).
VARIANT 600 600 K -> I (in strain EG5144).
VARIANT 624 624 K -> T (in strain EG5144).
VARIANT 65 79 Q -> P (in strain EG5144).
TURN 80 81 N -> D (in strain EG5144).
HELEX 83 86 I -> V (in strain EG5144).
TURN 87 88 F -> S (in strain EG5144).
HELEX 91 98 VVL -> IYF (in strain EG5144).
TURN 99 99 S -> G (in strain EG5144).
TURN 102 103 L -> I (in strain EG5144).
TURN 105 113 K -> I (in strain EG5144).
TURN 114 114 K -> T (in strain EG5144).
HELEX 115 118 Q -> P (in strain EG5144).
TURN 119 119 N -> D (in strain EG5144).
HELEX 124 153 I -> V (in strain EG5144).
HELEX 156 158 F -> S (in strain EG5144).
HELEX 161 181 VVL -> IYF (in strain EG5144).
TURN 182 185 S -> G (in strain EG5144).
TURN 188 189 L -> I (in strain EG5144).
TURN 191 209 K -> I (in strain EG5144).
TURN 210 210 K -> T (in strain EG5144).
HELEX 211 215 Q -> P (in strain EG5144).
TURN 216 220 N -> D (in strain EG5144).
HELEX 223 254 I -> V (in strain EG5144).
TURN 255 255 F -> S (in strain EG5144).
HELEX 260 276 VVL -> IYF (in strain EG5144).
TURN 277 277 S -> G (in strain EG5144).
HELEX 278 281 L -> I (in strain EG5144).

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FT TURN 282 283
FT TURN 284 287
FT TURN 289 294
FT STRAND 296 297
FT STRAND 304 305
FT TURN 313 315
FT HELIX 316 318
FT HELIX 322 326
FT TURN 327 328
FT STRAND 336 348
FT TURN 351 352
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FT STRAND 551 556
FT HELIX 559 562
FT STRAND 565 574
FT STRAND 578 584
FT TURN 585 586
FT STRAND 589 594
FT TURN 600 601
FT HELIX 606 608
FT STRAND 610 613
FT STRAND 618 619
FT STRAND 625 631
FT TURN 636 637
FT STRAND 640 649
SQ SEQUENCE 652 AA; 74385 MW; 63048332CDB8CCC6 CRC64;

Query Match 100.0%; Score 3406; DB 1; Length 652;
Best Local Similarity 100.0%; Pred. No. 2.3e-214;
Matches 652; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPNNSEHDTIKVTNSELQTHNQYPLADNPNSTLEELNYKEFLMTEDSDSTEVLDS 60
DB 1 MNPNNSEHDTIKVTNSELQTHNQYPLADNPNSTLEELNYKEFLMTEDSDSTEVLDS 60
QY 61 TVKDAVGTGIVSVGQILGVVGVFPAGALTFSFYQSFLNTIWPSDADPWKAFMAQVEVLIDK 120
DB 61 TVKDAVGTGIVSVGQILGVVGVFPAGALTFSFYQSFLNTIWPSDADPWKAFMAQVEVLIDK 120
QY 121 KIBEYAKSALAELOGLQNNFEDYVNALNSWKKTPLSLRSKRSDRIREFLSQAESHFRN 180
DB 121 KIBEYAKSALAELOGLQNNFEDYVNALNSWKKTPLSLRSKRSDRIREFLSQAESHFRN 180
QY 181 SMPSFAVSKPEVLFLPTYAQAAANTHLLLLKDAQVFGEEWGYSSSEDVAEFYHROLKLTQY 240
DB 181 SMPSFAVSKPEVLFLPTYAQAAANTHLLLLKDAQVFGEEWGYSSSEDVAEFYHROLKLTQY 240

241 TDHCVMWYVGLNGLRGSTYDAWKFNRFREMTLTVLDLIVLPFFDIRLYSGVKTEL 300
241 TDHCVMWYVGLNGLRGSTYDAWKFNRFREMTLTVLDLIVLPFFDIRLYSGVKTEL 300
301 TRDIFTDPIFSLNTLOEYGTPTFLSIENSIRKPHLFDYLGQIEFHTRLOQPGYFKDSFNYW 360
301 TRDIFTDPIFSLNTLOEYGTPTFLSIENSIRKPHLFDYLGQIEFHTRLOQPGYFKDSFNYW 360
361 SGNVETRPSIGSKTITSPFYGDKSTPEVKLSFDGQKVYRTTANTDVAWPNKGYVLG 420
361 SGNVETRPSIGSKTITSPFYGDKSTPEVKLSFDGQKVYRTTANTDVAWPNKGYVLG 420
421 VTKVDSQYDDQKNETSTQTYDSKRNNGHVSAODSIDQLPETTDEPLEKAYSHQLNYAE 480
421 VTKVDSQYDDQKNETSTQTYDSKRNNGHVSAODSIDQLPETTDEPLEKAYSHQLNYAE 480
481 CFLMDRRRGTPPFTWTHRSVDFNTIDAEKITQLPVVKAYALSSGASIIIEGPGFTGGL 540
481 CFLMDRRRGTPPFTWTHRSVDFNTIDAEKITQLPVVKAYALSSGASIIIEGPGFTGGL 540
541 LFLKESNSIAKEFKVTLNSAALLQRYVRIRYASTTNLRLFVQNSNDELVIYINKTMNK 600
541 LFLKESNSIAKEFKVTLNSAALLQRYVRIRYASTTNLRLFVQNSNDELVIYINKTMNK 600
601 DDDLTYQTFLATNSNMFGSGDKNELIIGAEFVSNEKIYIDKIEFIPVOL 652
601 DDDLTYQTFLATNSNMFGSGDKNELIIGAEFVSNEKIYIDKIEFIPVOL 652

RESULT 2
C3BA_BACTO STANDARD; PRT; 659 AA.
AC P17929;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cry3Ba (Insecticidal delta-endotoxin
DE CryIIIB(a)) (Crystalline entomocidal protoxin) (75 kDa crystal
DE protein)
GN Names=cry3Ba; Synonyms=cryIIb, cryIIIB(a);
OS Bacillus thuringiensis (subsp. tolworthi).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1442;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=43F;
RX MEDLINE=90206811; PubMed=2320431;
RA Sick A., Gaertner F.H., Wong A.;
RT "Nucleotide sequence of a coleopteran-active toxin gene from a new
RT isolate of Bacillus thuringiensis subsp. tolworthi.";
RL Nucleic Acids Res. 18:1305-1305(1990).
CC -|- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of Coleoptera.
CC -|- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -|- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -|- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X17123; CAA34983.1; -.
CC EMBL; A07234; CAA00645.1; -.
CC PIR; S10228; S10228.
CC HSSP; Q06117; 1J16.
CC InterPro; IPR001178; Endotoxin.

```

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DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
SQ SEQUENCE 659 AA; 75159 MW; 5ASB214FPB94168CA CRC64;

Query Match          94.3%; Score 3212; DB 1; Length 659;
Best Local Similarity 93.7%; Pred. No. 1.2e-201;
Matches 610; Conservative 22; Mismatches 19; Indels 0; Gaps 0;

QY 1 MNPNNRSHDITKVTPESELQNHQYPLADNPSTLEELNYKEPLRMTESSTVLDSN 60
DB 9 MNPNNRSEYDTTKVTPESELQNHQYPLADNPSTLEELNYKEPLRMTADNSTEVLDS 68

QY 61 TVKDAVGTGISVVGQILGVGVPPFAGALTSFYQSFLNTIWPSDADPWKAFMAQVLELIDK 120
DB 59 TVKDAVGTGISVVGQILGVGVPPFAGALTSFYQSFLNFWPSDADPWKAFMAQVLELIDK 128

QY 121 KIEEYAKSKALAELOGLQNNFEDYVNALNSWKKTPLSLRSKRQDRIRLELSQAESHFRN 180
DB 129 KIEEYAKSKALAELOGLQNNFEDYVNALDSWKKAPVNLRSRQDRIRLELSQAESHFRN 188

QY 181 SMPFAVSKFEVLPLPTVQAQAANTHLILLKDAQVGEWGYSSDVAEYHROLKLTQOY 240
DB 189 SMPFAVSKFEVLPLPTVQAQAANTHLILLKDAQVGEWGYSSDIAEYFQROLKLTQOY 248

QY 241 TDHCNVNNGVNLGRGTYDAWVFNRRREMTLTVDLIVLFFPYDIRLYSKGVKTEL 300
DB 249 TDHCNVNNGVNLGRGTYDAWVFNRRREMTLTVDLIVLFFPYDRLYLYSKGVKTEL 308

QY 301 TRDIFTDPIFSLNTLOEYGPFTFLSIENSRKPHLFDYLGIEFHTRLQPGYFGKDSFNWY 360
DB 309 TRDIFTDPIFSLNTLOEYGPFTFLSIENSRKPHLFDYLRGIEFHTRLRPGYFGKDSFNWY 368

QY 361 SGNYVETRISGSSKTIISPFYCDKSTEPVKLSFDGQKVVTIANTDVAAMPNCKVYIG 420
DB 369 SGNYVETRISGSSKTIISPFYCDKSTIEPIKLSFDGQKVVTIANTDVAAMPNCKVYIG 428

QY 421 VTKVDPFSQYDDQKNETSTQYDSKRNNGHVSAQDSIDQLPPTTDEPLEKAYSHQNLVAYE 480
DB 429 VTKVDPFSQYDDQKNETSTQYDSKRYNGYLGAQDSIDQLPPTTDEPLEKAYSHQNLVAYE 488

QY 481 CFIMQDRRTGTFPFTWTHRSVDFNTIDAETKLTQLPVVKAYALSSGASIEGPGTGGNL 540
DB 489 CFIMQDRRTGTFPFTWTHRSVDFNTIDAETKLTQLPVVKAYALSSGASIEGPGTGGNL 548

QY 541 LFLKSSNSIAKFKVTLNSAALLQRYVRIRVASTTNLRLFVQNSNNDPLVIYINKTMNK 600
DB 549 LFLKSSNSIAKFKVTLNSAALLQRYVRIRVASTTNLRLFVQNSNNDPLVIYINKTMNK 608

QY 601 DDDLTQTQFDLATTNSNMFGSDGKNEILIGAESFVSNEKIYIDKIEFIPVQ 651
DB 609 DGDLTQTQFDLATTNSNMFGSDGTDNFIIGAESFVSNEKIYIDKIEFIPVQ 659

RESULT 3
C3AA_BACTT
ID_C3AA_BACTT STANDARD; PRT; 644 AA.
AC P07130; 212255;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE Pesticidal crystal protein cry3Aa precursor (Insecticidal delta-
DE endotoxin CryIIIA(a)) (Crystalline entomocidal protoxin) (73 kDa
DE crystal protein).
GN Names-cry3Aa; Synonyms-bt13, cry3A, cryC, cryIIIA, cryIIIA(a);
OS Bacillus thuringiensis (subsp. tenebrionis),
OS Bacillus thuringiensis (subsp. morrisoni), and
OS Bacillus thuringiensis (subsp. san diego).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
```

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OX NCBI_TaxID=1444, 1441, 1435;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.tenebrionis;
RX MEDLINE=88015559; PubMed=3658680;
RA Hoesfte H., Seurinck J., Houtven A.V., Vaeck M.;
RT "Nucleotide sequence of a gene encoding an insecticidal protein of
RT Bacillus thuringiensis var. tenebrionis toxic against Coleoptera.";
RL Nucleic Acids Res. 15:7183-7183(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.tenebrionis;
RA Sekar V., Thompson D.V., Maroney M.J., Bookland R.G., Adang M.J.;
RT "Molecular cloning and characterization of the insecticidal crystal
RT protein gene of Bacillus thuringiensis var. tenebrionis.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:7036-7040(1987).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.tenebrionis;
RA McPherson S.A., Perlak F.J., Fuchs R.L., Marrone P.G., Lavrik P.B.,
RA Fischhoff D.A.;
RT "Characterization of the coleopteran-specific protein gene of Bacillus
RT thuringiensis var. tenebrionis.";
RL Biotechnology (N.Y.) 6:61-66(1988).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.tenebrionis; STRAIN=NB176;
RX MEDLINE=95131759; PubMed=7830581;
RA Adams L.F., Mathewes S., O'Hara P., Petersen A., Gurtler H.;
RT "Elucidation of the mechanism of CryIIIA overproduction in a
RT mutagenized strain of Bacillus thuringiensis var. tenebrionis.";
RL Mol. Microbiol. 14:381-389(1994).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.tenebrionis; STRAIN=EG2158;
RX MEDLINE=89111239; PubMed=3146015;
RA Donovan W.P., Gonzalez J.M. Jr., Gilbert M.P., Dankocsik C.C.;
RT "Isolation and characterization of EG2158, a new strain of Bacillus
RT thuringiensis toxic to coleopteran larvae, and nucleotide sequence of
RT the toxin gene.";
RL Mol. Gen. Genet. 214:365-372(1988).
RN [6]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.san diego;
RX MEDLINE=88112860; PubMed=1658659; DOI=10.1016/0378-1119(87)90174-0;
RA Hernstadt C., Gilroy T.E., Sobieski D.A., Bennett B.D.,
RA Gaertner F.H.;
RT "Nucleotide sequence and deduced amino acid sequence of a coleopteran-
RT active delta-endotoxin gene from Bacillus thuringiensis subsp. san
RT diego.";
RL Gene 57:37-46(1987).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RC SPECIES=B.t.tenebrionis;
RX MEDLINE=92049729; PubMed=1658659; DOI=10.1038/353815a0;
RA Li J., Carroll J., Ellar D.J.;
RT "Crystal structure of insecticidal delta-endotoxin from Bacillus
RT thuringiensis at 2.5-A resolution.";
RL Nature 353:815-821(1991).
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of Coleoptera.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- BIOTECHNOLOGY: Introduced by genetic manipulation and expressed in
CC insect-resistant potato by Monsanto.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
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CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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Q9SG69	Q9SG69	PRELIMINARY;	PRT;	652 AA.
ID	Q9SG69;			
AC	01-MAY-2000 (TremBLrel. 13, Created)			
DT	01-MAY-2000 (TremBLrel. 13, Last sequence update)			
DT	01-MAY-2000 (TremBLrel. 26, Last annotation update)			
DE	Cry3Aa protein.			
GN	Name=cry3Aa;			
OS	Bacillus thuringiensis.			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=1428;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Bt22;			
RA	Zhang J., Song F.P., Xie T.J., Wang K.M., Huang D.F.;			
RL	Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; A2737900; CAB41411.1; -			
DR	PIR; A27323; A27323.			
DR	HSSP; P07130; IDLC.			
DR	GO; GO:0005102; F:receptor binding; IEA.			
DR	GO; GO:0006952; P:defense response; IEA.			
DR	GO; GO:0009405; P:pathogenesis; IEA.			
DR	InterPro; IPR001178; Endotoxin.			
DR	InterPro; IPR005638; endotoxin_C.			
DR	InterPro; IPR008979; Gal_bind_like.			
DR	Pfam; PF03944; Endotoxin_C; 1.			
DR	Pfam; PF00555; Endotoxin_M; 1.			
DR	Pfam; PF03945; Endotoxin_N; 1.			
SQ	SEQUENCE 652 AA; 544AE16E1DDF7647 CRC64;			
Query Match 68.7%; Score 2341.5; DB 2; Length 652;				
Best Local Similarity 68.6%; Pred. No. 1.1e-144;				
Matches 446; Conservative 75; Mismatches 122; Indels 7; Gaps 6;				
QY	1	MNPNRSEHDTTKVTNSELQTNHNYQPLADNPNSTLELNKYKEFLRMTEDSSTEVLDS	60	
DB	9	MNPNRSEHDTTKTENNEVPTNHVQYPLAETPNPTLEDLNKYKEFLRMTADNNTALDSS	68	
QY	61	TVKDAVGTGIVVGQILGVGVFPFAGALTSFYQSFLNTIWPSDADPWKAFMAQVEVLIDK	120	
DB	69	TTKDVITQKGISVVGDLGVGVFPFGALVSFTNFLTNIWPE-DPWKAFMEQVEALMDQ	127	
QY	121	KIEEYAKSALAEQLQGNFEDYVNALNSWKKTPLSLRSKRSQDRIRLEFSAQSHFRN	180	
DB	128	KIADYAKNKAELAEQLQGNVEDYVSALSSWQKNPVSSRNPHSQGRIRLEFSAQSHFRN	187	
QY	181	SMPSFAVSKEVLFPLTYAQAANTHLLKDAQVGEWGYSSDVAEFYHRLKLTQOY	240	
DB	188	SMPSFAISGYEVLFTTYAQAANTHLLKDAQIYGEWGYEKEDIAEFYKRLKLTQOY	247	
QY	241	TDHCNVNNGVGLRGSTYDAWKVFNRRREMTLVLDLIVLPFYDIRLYSKGVKTEL	300	
DB	248	TDHCNVNNGVGLKRGSSYESWVNFNRYRREMTLVLDLIALFPLYDVRLYPKVKTEL	307	
QY	301	TRDIFDTPFISLNTLOEYGPTELSENIRKPHLFDYLOQIEPHTLQPGYFGKDSFNW	360	
DB	308	TRDVLTDPIVGVNLRGVTTFNENIRKPHLFDYLRHQHTFQPGYGYGNDSPFNW	367	
QY	361	SGNYVETRPSIGSKTTSPFYGDKSTEPVKLSFDGQKVYRTIANTDVAAMPNGKVYLG	420	
DB	368	SGNYVETRPSIGSNDIITSPFYGNKSSPEVQNLEFNGEKVYRAVANTNLAVWPSA-VYSG	426	
QY	421	VTKVDFSOYDDQKNETSTQTYDSKRNHVSQAODSIDOLPPETTDEPLEKAYSHQLNAYE	480	
DB	427	VTKVEFSQYNDQDEASTQTYDSKRNVGVS-WDSIDQLPPETTDEPLEKAYSHQLNAYE	485	
QY	481	CFLMQDRRGTHPFTWTHRSVDVFNTIDAEKITQLPVRKAYALSSGASIEGGPFTGNL	540	
DB	486	CFLMQSGRGIHPVLTWTHKSDVFNNMDSKKITQLPVRKAYLKQSGASVVGPRFTGGDI	545	
QY	541	LFLKSSNSNAKPKVTLNSAALLQRYVRIRYASTNLRFLFVQNSNNDFLIIVYINTKMK	600	

546	IQCTE-NGSAAITYVT-PDVSVSQKPARIHVASTSQITFTLSLDGAPNQYYPDKTINK	603
601	DDDLTYQTFDLATNTSGMFGSGDKNELIIGAESFVSNENKIYIDKIEFIPV	650
604	GDTLITYNSFNLASFSFPFELSG--NNLQIGVTGLSAGDKVYIDKIEFIPV	651

RESULT 5			
Q6PXN8	PRELIMINARY;	PRT;	652 AA.
ID	Q6PXN8;		
AC	05-JUL-2004 (TremBLrel. 27, Created)		
DT	05-JUL-2004 (TremBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TremBLrel. 27, Last annotation update)		
DE	Insecticidal crystal protein.		
GN	Name=cry3;		
OS	Bacillus thuringiensis.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=1428;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=YM-03;		
RA	Gao M., Cai Y.;		
RL	Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY572010; AAS79487.1; -		
DR	GO; GO:0005102; F:receptor binding; IEA.		
DR	GO; GO:0006952; P:defense response; IEA.		
DR	GO; GO:0009405; P:pathogenesis; IEA.		
DR	InterPro; IPR001178; Endotoxin.		
DR	InterPro; IPR005638; endotoxin_C.		
DR	InterPro; IPR008979; Gal_bind_like.		
DR	Pfam; PF03944; Endotoxin_C; 1.		
DR	Pfam; PF00555; Endotoxin_M; 1.		
DR	Pfam; PF03945; Endotoxin_N; 1.		
SQ	SEQUENCE 652 AA; 74007 MW; AC2756FDED104A45 CRC64;		
Query Match 68.6%; Score 2337.5; DB 2; Length 652;			
Best Local Similarity 68.5%; Pred. No. 1.9e-144;			
Matches 445; Conservative 76; Mismatches 122; Indels 7; Gaps 6;			
QY	1	MNPNRSEHDTTKVTNSELQTNHNYQPLADNPNSTLELNKYKEFLRMTEDSSTEVLDS	60
DB	9	MNPNRSEHDTTKTENNEVPTNHVQYPLAETPNPTLEDLNKYKEFLRMTADNNTALDSS	68
QY	61	TVKDAVGTGIVVGQILGVGVFPFAGALTSFYQSFLNTIWPSDADPWKAFMAQVEVLIDK	120
DB	69	TTKDVITQKGISVVGDLGVGVFPFGALVSFTNFLTNIWPE-DPWKAFMEQVEALMDQ	127
QY	121	KIEEYAKSALAEQLQGNFEDYVNALNSWKKTPLSLRSKRSQDRIRLEFSAQSHFRN	180
DB	128	KIADYAKNKAELAEQLQGNVEDYVSALSSWQKNPVSSRNPHSQGRIRLEFSAQSHFRN	187
QY	181	SMPSFAVSKEVLFPLTYAQAANTHLLKDAQVGEWGYSSDVAEFYHRLKLTQOY	240
DB	188	SMPSFAISGYEVLFTTYAQAANTHLLKDAQIYGEWGYEKEDIAEFYKRLKLTQOY	247
QY	241	TDHCNVNNGVGLRGSTYDAWKVFNRRREMTLVLDLIVLPFYDIRLYSKGVKTEL	300
DB	248	TDHCNVNNGVGLKRGSSYESWVNFNRYRREMTLVLDLIALFPLYDVRLYPKVKTEL	307
QY	301	TRDIFDTPFISLNTLOEYGPTELSENIRKPHLFDYLOQIEPHTLQPGYFGKDSFNW	360
DB	308	TRDVLTDPIVGVNLRGVTTFNENIRKPHLFDYLRHQHTFQPGYGYGNDSPFNW	367
QY	361	SGNYVETRPSIGSKTTSPFYGDKSTEPVKLSFDGQKVYRTIANTDVAAMPNGKVYLG	420
DB	368	SGNYVETRPSIGSNDIITSPFYGNKSSPEVQNLEFNGEKVYRAVANTNLAVWPSA-VYSG	426
QY	421	VTKVDFSOYDDQKNETSTQTYDSKRNHVSQAODSIDOLPPETTDEPLEKAYSHQLNAYE	480
DB	427	VTKVEFSQYNDQDEASTQTYDSKRNVGVS-WDSIDQLPPETTDEPLEKAYSHQLNAYE	485
QY	481	CFLMQDRRGTHPFTWTHRSVDVFNTIDAEKITQLPVRKAYALSSGASIEGGPFTGNL	540
DB	486	CFLMQSGRGIHPVLTWTHKSDVFNNMDSKKITQLPVRKAYLKQSGASVVGPRFTGGDI	545
QY	541	LFLKSSNSNAKPKVTLNSAALLQRYVRIRYASTNLRFLFVQNSNNDFLIIVYINTKMK	600

Db	546	IQCTE-NGSAATYYVT-PDVVSQYKVRARIHVASTSQITFTLSLDGAPNPQYYPDKTINK	603
Qy	601	DDDLTYQTFLDATTNMGMFGSGDKNELIIGAESFVSNKIKYIDKIEFIPV	650
Db	604	GDLTLYNSFNIAFSFTPELSG--NNLQIGVTGLSAGDKVYIDKIEFIPV	651
RESULT 5			
ID	Q6PXN8	PRELIMINARY; PRT; 652 AA.	
AC	Q6PXN8;		
DT	05-JUL-2004 (Tremblrel. 27, Created)		
DT	05-JUL-2004 (Tremblrel. 27, Last sequence update)		
DE	05-JUL-2004 (Tremblrel. 27, Last annotation update)		
DE	Insecticidal crystal protein.		
GN	Name=cry3;		
OS	Bacillus thuringiensis.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=1428;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=YM-03;		
RA	Gao M., Cai Y.;		
RL	Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY572010; AAS79487.1; --		
DR	GO; GO:0005102; F:receptor binding; IEA.		
DR	GO; GO:0006952; P:defense response; IEA.		
DR	GO; GO:0009405; P:pathogenesis; IEA.		
DR	InterPro; IPR001178; Endotoxin.		
DR	InterPro; IPR005638; endotoxin_C.		
DR	InterPro; IPR008979; Gal_bind_like.		
DR	Pfam; PF03944; Endotoxin_C; 1.		
DR	Pfam; PF00555; Endotoxin_M; 1.		
DR	Pfam; PF03945; Endotoxin_N; 1.		
SQ	SEQUENCE 652 AA; 74007 MW; AC2756FDEBD104A45 CRC64;		
Query Match 68.6%; Score 2337.5; DB 2; Length 652;			
Best Local Similarity 68.5%; Pred. No. 1.9e-144;			
Matches 445; Conservative 76; Mismatches 122; Indels 7; Gaps 6;			
Qy	1	MNPNRSEHDTIKVTNSELQTNHNYQPLADNPNSTLELNKYKEFLRMTEDSSTEVLDS	60
Db	9	MNPNRSEHDTIKTENNEVPTNHVQYPLAETNPPTLEDLNKYKEFLRMTADNTEALDSS	68
Qy	61	TVKDAVGTSVVGQILGVGVFPFAGALTSFYQSFLNTIWPSDADPWKAFMAQVEVLIDK	120
Db	69	TTKDVQIGKISVVGDLGVGVFPFGGALVSFTNFLTNIWPE-DPWKAFMEQVEALMDQ	127
Qy	121	KIEEYAKSALAEQLQGNFEDYVNALNSWKKTPLSLRSKSQDRIRLEFSAQSHFRN	180
Db	128	KIADYAKNKAELAEQLQGNVEDYVSALSSWQKNPVSSRNPHSQGRIRLEFSAQSHFRN	187
Qy	181	SMPSFAVSKEVLFPLTYAQAANTHLLKDAQVGEWGYSSDVAEFYHRLKLTQOY	240
Db	188	SMPSFAISGYEVLFTTYAQAANTHLLKDAQIYGEWGYEKEDIAEFYKRLKLTQOY	247
Qy	241	TDHCNVNNGVGLRGSTYDAWKVFNRRREMTLVLDLIVLPFYDIRLYSKGVKTEL	300
Db	248	TDHCNVNNGVGLKRGSSYESWVNFNRYRREMTLVLDLIALFPLYDVRLYPKVKTEL	307
Qy	301	TRDIFDTPFISLNTLOEYGPTELSENIIRKPHLFDYLOQIEPHTLQPGYFGKDSFNW	360
Db	308	TRDVLTDPIVGVNLRGVTTFNENIIRKPHLFDYLRHQHTFQPGYGYGNDSPFNW	367
Qy	361	SGNYVETRPSIGSSKTTSPFYGDKSTEPVKLSFDGQKVYRTIANTDVAAMPNGKVYLG	420
Db	368	SGNYVETRPSIGSNDIITSPFYGNKSSPEVQNLEFNGEKVYRAVANTNLAVWPSA-VYSG	426
Qy	421	VTKVDFSOYDDQKNETSTQTYDSKRNHVSQAODSIDOLPPETTDEPLEKAYSHOLNYAE	480
Db	427	VTKVEFSQYNDQDEASTQTYDSKRNVGAVS-WDSIDQLPEPPTTDEPLEKAYSHOLNYAE	485

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Qy 481 CFLMQDRRGTPFTWTHRSYDFNTTDAEKITQLPVVKAYALSSGASIIIEGFGTGGNL 540
Db 486 CFLMQSGRGTPVLTWTHKSVDFNMDISKKITQLPLVKAYQLSGASVAVGRFTGGDI 545
Qy 541 LFLKESNSAKFKVTLNSAALLQRYVRIRYASTTNLRLFVQNSNNDFLVIYINKTMNK 600
Db 546 IQCTE-NGSAATIVT-PDVSYSQKRRARIHYASTSQITFTLSLDGAPFNQYFDKTIK 603
Qy 601 DDLLTYQTFDLATNSNMGFGDKNELIIGAESFVSNKEIYIDKIEPIV 650
Db 604 GDILTYSNPNLASFSTPFELSG--NNLQIGVTGLSAGDKYIDKIEPIV 651

RESULT 6
Q64327 PRELIMINARY; PRT; 652 AA.
AC Q64327
DT 23-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Cry3Aa protein.
GN Names: cry3Aa.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=886;
RA Chen J., Dai L.-Y., Wang X.-P., Tian Y.-C., Lu M.-Z.;
RT "A cry3Aa gene from Bacillus thuringiensis Bt886 encoding the toxin
RL against long-horned beetles.";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY728479; AAU29411.1; -.
SQ SEQUENCE 652 AA; 74033 MW; BB3628471D0FFA27 CRC64;

Query Match 68.1%; Score 2319.5; DB 2; Length 652;
Best Local Similarity 68.0%; Pred. No. 2.9e-143;
Matches 442; Conservative 77; Mismatches 124; Indels 7; Gaps 6;

Qy 1 MNPNNRSEHDTIKVTPNSELOTHNHOYPLADNPNSTLEELNYKEFLRMTEDSSTEVLDNS 60
Db 9 MNPNNRSEHDTIKVTENNEVPTNHOYPLAETNPFTLEDNLNYKEFLRMADNNTEALDSS 68

61 TVKDAVGTGIVSVGQILGVGVFPAGALTSFYOSFLNTIWPSDADPWKAPMAQVVLIDK 120
69 TTKDVIQKGLSVGDLGVGFPGGALVSFYTNFLNTIWPSE-DPWKAPMEQVEALMDQ 127

121 KIEYAKSKALAEQLQGNFEDYVNALNSWKTKTPLSLRSQDRIRELFSQAESHFRN 180
128 KIADYAKNKALAEQLQGNVEDYVLSWQKNPVSSRNPHSQGRIRELFSQAESHFRN 187

181 SMPSEAVSKFEVLFLPTAYAAANTHLLLLKDAQVGEWGYSEDVAEFVHROLKLTQY 240
188 SMPSEALSGYEVFLFTTYAQAANIHLPLKDKAQIYGEWGYEKEDAEAFYKROLKLTQY 247

241 TDCVNMVNYGLNGRGSTYDAWKFNFRPREMTLTVLDLIVFPFYDIRLYSGVKTEL 300
248 TDCVKNVYVGLDKRGSSYSEWVFNRYREMTLTVLDLIALFPYLDVRLYKVKTEL 307

301 TRDIFTDPIPSLNTLOEYGTFFLSIENSIRKPHLFYDLQIEFTHRLQPGYFGKDSFNW 360
308 TRDVLTDPIVGNVNLRCYGTFFSNIENIRKPHLFYDLHRIQPHTRFRPGYGNDSFNW 367

361 SGNVVTSPISGSKTITSFYGDKSTEPVKLSFGQKVVRTIANTDVAAWNGKYYLG 420
368 SGNVVTSPISGNDIITSFYGNKSEFPVONLEFNGEKYRVAVANTNLAVWPSA-VYSG 426

421 VTKVDFSQYDDQKNSTQYDYSKRNNGHVSAQDSIDQLPPTETDPELEKAYSHQNYAE 480
427 VTKVFSQYNDQYDEASTQYDYSKRVGAVS-WDSIDQLPPTETDPEPEKGYSHQNYM 485

481 CFLMQDRRGTPFTWTHRSYDFNTTDAEKITQLPVVKAYALSSGASIIIEGFGTGGNL 540
Db 486 CFLMQSGRGTPVLTWTHKSVDFNMDISKKITQLPLVKAYQLSGASVAVGRFTGGDI 545
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Db 486 CFLMQSGRGTPVLTWTHKSVDFNMDISKKITQLPLVKAYQLSGASVAVGRFTGGDI 545
Qy 541 LFLKESNSAKFKVTLNSAALLQRYVRIRYASTTNLRLFVQNSNNDFLVIYINKTMNK 600
Db 546 IQCTE-NGSAATIVT-PDVSYSQKRRARIHYASTSQITFTLSLDGAPFNQYFDKTIK 603
Qy 601 DDLLTYQTFDLATNSNMGFGDKNELIIGAESFVSNKEIYIDKIEPIV 650
Db 604 GDILTYSNPNLASFSTPFELSG--NNLQIGVTGLSAGDKYIDKIEPIV 651

RESULT 7
C3CA_BACTK STANDARD; PRT; 649 AA.
AC Q45744;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cry3Ca (Insecticidal delta-endotoxin
DE CryIIIC(a)) (Crystalline entomocidal protoxin) (73 kDa crystal
DE protein).
GN Name: cry3Ca; Synonyms: cryIIIC(a), cryIIId;
OS Bacillus thuringiensis (subsp. kurstaki).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bt1109P;
RX MEDLINE=92184108; PubMed=1544571; DOI=10.1016/0378-1119(92)90457-2;
RA Lambert B., Theunis W., Aguda R., Van Audenhove K., Decock C.,
RA Jansens S., Seurinck J., Peferoen M.;
RT "Nucleotide sequence of gene cryIIId encoding a novel coleopteran-
RT active crystal protein from strain Bt1109P of Bacillus thuringiensis
RT subsp. kurstaki.";
RL Gene 110:131-132(1992).
CC -I- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut
CC epithelial cells of Coleoptera.
CC -I- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -I- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -I- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X59797; CAA42469.1; -.
CC FIR; JH0261; JH0261.
CC HSSP; P07130; 1DLIC.
CC InterPro; IPR001178; Endotoxin.
CC InterPro; IPR005638; endotoxin_C.
CC InterPro; IPR005639; endotoxin_N.
CC InterPro; IPR008979; Gal_bind_like.
CC Pfam; PF03944; Endotoxin_C; 1.
CC Pfam; PF00555; Endotoxin_M; 1.
CC Pfam; PF03945; Endotoxin_N; 1.
CC Sporulation; Toxin.
CC SEQUENCE 649 AA; 73026 MW; 8FF1F0B47957AC49 CRC64;

Query Match 63.2%; Score 2152; DB 1; Length 649;
Best Local Similarity 62.2%; Pred. No. 2.7e-132;
Matches 407; Conservative 95; Mismatches 142; Indels 10; Gaps 6;

Qy 1 MNPNNRSEHDTIKVTPNSELOTHNHOYPLADNPNSTLEELNYKEFLRMTEDSSTEVLDNS 60
Db 1 MNPNNRSEHDTIKATENNEVSNHNAHQYPLADTP--TLEELNYKEFLRTTDDNNVEALDSS 58
```



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Qy 61 TVKDAVGTGISVWGQILGVGVPPFAGALTSTFYQSFLNTIWPSDADPWKAFMAQVEVLIDK 120
Db 59 TTKDAIQKISIGDILGVGVPPYGCALVSFYTNLLNTIWPCE-DPLKAFMQQVEALIDQ 117

Qy 121 KIEEYAKSALAELQGLQNNFEDYVNALNSKKTPLSLRKSQDRIRBELFSQAESHPFN 180
Db 118 KIADYAKAKATAELOGLKQNVKDYVSALDSMDKTPLTLLDGRSQGRIRBELFSQAESHPFR 177

Qy 181 SMPSEAVSKFEVLFTPTVAQAANTHLLLLKDAQVFGEEGWSSYSEDVAFYHRLKLTQOY 240
Db 178 SMPSEAVSGYEVLFPTVAQAANTHLLLLKDAQIYGTGWDGISTDDLNEFEHTKQKDLTIEY 237

Qy 241 TDHCNVNVNGLNGLRGSTDYDAWVKNRFRREMTLTVLDLIVLFPFYDIRLYSKGVKTEL 300
Db 238 TNHCAKWKAGLDKLRGSTYEYEWKFNRYRREMTLTVLDLITLFLPYDYVRTYTKGVKTEL 297

Qy 301 TRDITFDPIFSLNTLQEGVPTLSLSTENSRKPKHFDYLGQIEFHTRLQPGYFGKDSFNW 360
Db 298 TRDVLTDPIVAVNNWNGYGTTFNSIENYIRKPKHFDYLAHQFHSRLQPGYFGTDSFNW 357

Qy 361 SGNVETRPSIGSSKTIITSPFYGDKSTPEVQKLSFDGQKQVYRTIANTDVAWPNQ----K 416
Db 358 SGNVYSTRSSIGSDEIIRSPFYGNKSTLDVQNLFEENGKVFRAVANGNLAVPVGCTGK 417

Qy 417 VILGVTKVDFSQYDDOKNETSTQYDSKKNHGVSAQDSIDOLPPTTDEPLEKAYSQOL 476
Db 418 IHSQVTKVQFSQYNDKRDVRTQYDSKKNVGGI-VFDSIDQLPPTTDESLEKAYSQOL 476

Qy 477 NYAECFLMDRRRTIPFFTWTHRSVDFNTIDAETIOLPVVKAYALSSGASIIIRGPGFT 536
Db 477 NVYRCFLQGRGIIIPVFTWTHKSVDFYNTLJSEKITQIPFVKAFILVNSTSVVAGPGFT 536

Qy 537 GGNLLFLKSSNSIAKPKVTLNSAALLQRYVRIRYASTNRLRFVQNSNDFLVIYNK 596
Db 537 GGDIIKCTNGS-GLTLVYTPAPDLTYSKYKIRYASTSQVRFGIDLGSTHYSYFDK 595

Qy 597 TNNKDDDLTYQTFDLATNNSMGFCGDKNELIIGAESFVSNKIKYIDKIEFIPV 650
Db 596 TMDKGNLTNTYNSPLNSVRPIEISGG-NKIGVSGGIGSGDEVIYIDKIEFIPM 648
```

```
RESULT 8
Q8KZL7
ID Q8KZL7 PRELIMINARY; PRT; 1144 AA.
AC Q8KZL7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cry8 protein.
GN Name-cry8;
OS Bacillus thuringiensis (subsp. galleriae).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29338;
RN [1]
RP SEQUENCE FROM N.A.
RC Asano S., Yamashita C., Iizuka T., Takeuchi K., Yamanaka S., Cerf D.,
RA "A strain of Bacillus thuringiensis subsp. galleriae containing a
RT novel cry8 gene highly toxic to Anomala cuprea (Coleoptera:
RT Scarabaeidae).";
RL Biol. Control 26:191-196(2003).
DR HSSP; A089299; BAC07226.1; -.
DR EMBL; AB06117; IJ16.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0009079; 4 helix cytokine.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
```

```
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1144 AA; 128060 MW; 98F93070C49014AB CRC64;

Query Match 37.4%; Score 1272.5; DB 2; Length 1144;
Best Local Similarity 40.9%; Pred. No. 2.1e-74;
Matches 284; Conservative 115; Mismatches 222; Indels 73; Gaps 19;

Qy 1 MNPNNREHTIKVTPNSEIQTNNHQPPLADNPSTLEELNYKEFLRMSTSDSSTVELDNS 60
Db 1 MSPNNQNEYIELDASSSTSVSDNSVRYPLANDQTTLLQNNMNYKDYLRMSGEENPELPGNP 60

Qy 61 TV---KDAVGTGISVWGQILGVGVPPAGALTSTFYQSFLNTIWPSD-ADPWKAFMAQVEV 116
Db 61 ETFISSSTVQTGIGVQVIGALGVPPAGQIASFYSFIVGLWPSSTVSVWEMIMKQVED 120

Qy 117 LIDKKIEYAKSALAELQGLQNNFEDYVNALNSKKTPLSLRKSQDRIREL-----FS 172
Db 121 LIDQKITDSVRKTAGALQGLDGLDVYQKSLKNWLE-----NRNDTRARSVVVTQYI 173

Qy 173 QAESHFRNSMPSFAVSKFEVLFTPTVAQAANTHLLLLKDAQVFGEEGWSSYSEDVAFVHR 232
Db 174 ALELDFAKIPSPFAISGOEVPPLLSVYAQAANLHLLLRDASIFGAENGFTPEGEISTYDR 233

Qy 233 QLKLTQQVTDHCVNNVNVNGLNGLRGSTDYDAWVKNRFRREMTLTVLDLIVLFPFYDIRLY 292
Db 234 QVTTAQYSDYCVKWKYNTGLDKLGTNAASWLKVHQPFRREMTLLVLDLVALFPNYDTRY 293

Qy 293 SKGVKTELTRDIFTDPI-----FSLNTLQEGVPTFLSIENS-IRKPKHLDYL 338
Db 294 PIETTAQLTREVTYDPIVFNRETSGGFCRRWSLNS-----DISFSEVESAVIRSHLFDIL 349

Qy 339 QGIEFH-TRLPQYFGKDSFNYSNGVYVETRPSIGSSK-----TITS---PFY--GDKS 386
Db 350 SEIEFYTTIRAGLPLNTEYLEYVWGHISIKYKYNWASSALERNYGTIISNKIKYIDLANKD 409

Qy 387 TEPQKLSFDQKQVYRTIANTDVAAPNGKVYLGVTKVDFSQYDDQKNETQTO--TYDSK 444
Db 410 IFQVRSLGADLANVY-----AQVY-GVPYASFLLDKNTGSGVGGFTSKP 455

Qy 445 RNNGHVSAQ--DSIDQLPPTTDEPLEKAYSQOLNYAECFLMQD-----RRGTIPPTW 496
Db 456 HTTWQVCTQNTYNTIDEIPPE--NEPLSRGYSHRLSHITSYFSKKNASSPARYGNLPVPAW 513

Qy 497 THRSVDFFNTIDAETIOLPVVKAYALSSGASIIIEGPGFTGCGNLIFLKSSNSIAKPKVT 556
Db 514 THRSADVNTVYSDKITQIPVVKAHTLVSGTVIKGPGFTGCGNIL-KRTSSGPLAYTSVS 572

Qy 557 LNSAALLQRYVRIRYASTNRLRFVQNSNDFLVIYNKWNKDDDLTYQTFDLATNNS 616
Db 573 VKS-PLSQRYRARIRYASTNRLRFVTISGTRIYSINYNKTNMKNKGGDLTFNTFDLATIGT 631

Qy 617 NMGFSGDKNELIIGAESFVSNKIKYIDKIEFIPV 650
Db 632 APTFSNYSDSLTVGADSPASGGEVYVDKPELIPV 665
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RESULT 9
C8AA_BACUK
ID C8AA_BACUK STANDARD; PRT; 1157 AA.
AC Q45704;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cry8Aa (insecticidal delta-endotoxin
DE CryVIIIa(a) (Crystalline entomocidal protoxin) (131 kDa crystal
DE protein).
GN Name-cry8Aa; Synonyms=cryVIIIa(a);
OS Bacillus thuringiensis (subsp. kumamotoensis).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=132267;
RN [1]
RP SEQUENCE FROM N.A.
```



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Db 61 EVFLSEQDAVKAADIIVGKLLTGLGVFPVGVPIVSLYTQILDILWFSKQSKQWEIWEQVE 120
Qy 116 VLIDKKIEYAKSALAELOGLONNFEDYVNALNSWKKTPLSLRSGRDRIRLEFSQAE 175
Db 121 ELINQKIAEYARNKALSEGLEGLNNYQLYLTAALEWKENPNSRALRD---VNRNFEILD 177
Qy 176 SHFRNSMPSFAVSKFEVLPLTYAQAANTHLLLLDKDAQVGEWGYSSDEVAEFVHRQLK 235
Db 178 SLFTQMPSPFRVTFNEVPELTYTAAANLHLLLDASIFGEWGLSTSTINNYNRQWK 237
Qy 236 LTQQYTDHCVMWYVGLNGLRGSTVDAMVKFRFRREMTLVLDLVLFPFFYDILYSGK 295
Db 238 LTAESDHCVKYETGLAKLKSSAKQWIDYQNPFRMTLVLDVVALFSNYDTTYPLA 297
Qy 296 VKTELTRDFTDP-----IFSANTLOEQYGTPLFSIEN-SIRKPHLFDYLOQIEFHTRLOP 349
Db 298 TTAQLTREYVTDPLGAVDVPNIGSWYDKAPSFSEIEKAAIRPPHVDYITGLTVTKRS 357
Qy 350 GYFGKDSF-NYHSGNYVETRPISGSKTITSPFYGDKSTEPVKLSFDGQKVYRTIANTD 408
Db 358 --FTSDRYMRYWAGHQISYK-HIGTSSTFTQMYGTQNLQSTSNFDFNYDIYKTLNSGA 414
Qy 409 V---AAWPNKGKY--LGVTKVDFSOYDDQKNETSTQTYDSKRNNGHVSAQDSIDOLPPE 463
Db 415 VLLDIVP-GYTYTFGMEPETEFFMVNQLNTRKLTLYKPAKDIIIDTRDSELELPET 473
Qy 464 TDEPLEKAYSHQNYAEACFLMDRRGTIPFTFTWTHRSVDFNTIDAETKITQLPVVKAYAL 523
Db 474 SGOPNYESYSHLGHITFTYSSSTSYVPVFSWTHRSADLTNTVKSGETIQPGGKSTI 533
Qy 524 SSGASIEGPGTGNLLFLKSSNSIAKPKYTLNSAALLORYVRIRYAS--TTNLRLF 581
Db 534 GRNTYIIRKGYTGDDVALTDRIQS-CFQMFPESS---QRFRIRIRYASNETSYISLY 589
Qy 582 VQNSNN--DPLVIYINKTNKDDLTQYTFD-----LATNSNMGFSGDKNELIIGAES 633
Db 590 GLNQSGTLKFNQYTSKNEN---DLYTDFKIEYPRVLSVNA---SSNIQRLSIGIQ- 641
Qy 634 FVSNEKIYI-DKIEFTIPV 650
Db 642 --TNTNLFIIDRIEFTIPV 657
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RESULT 11

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C9CA_BACTO STANDARD; PRT; 1157 AA.
ID C9CA BACTO
AC Q45733,
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cry9Ca (insecticidal delta-endotoxin
DE CryXC(a)) (Crystalline entomocidal protoxin) (130 kDa crystal
DE protein).
GN Name=cry9Ca; Synonyms=cryIXC(a);
OS Bacillus thuringiensis (subsp. tolworthii)
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1442;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=BTS02618A;
RX MEDLINE=96141404; PubMed=8572715;
RA Lambert B., Buysse L., Decock C., Janssens S., Piens C., Saey B.,
RA Seurinck J., Van Audenhove K., Van Rie J., Van Vliet A., Peferoen M.;
RT "A Bacillus thuringiensis insecticidal crystal protein with a high
RT activity against members of the family Noctuidae.";
RL Appl. Environ. Microbiol. 62:80-86(1996).
CC -!- FUNCTION: Promotes colloidotomic lysis by binding to the midgut
CC epithelial cells of Lepidoptera larvae. Has a fairly broad
CC spectrum of activity against members of the Pyralidae,
CC Plutellidae, Sphingidae and Noctuidae families. It was the first
CC insecticidal crystal protein characterized with activity against
CC cutworms. No activity is observed against some beetles, such as
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CC the Colorado potato beetle.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC
CC EMBL; Z37527; CAA85764.1; -.
CC PIR; A59350; S49247.
CC HSSP; P07130; 1DLC.
CC InterPro; IPR001178; Endotoxin.
CC InterPro; IPR005638; endotoxin_C.
CC InterPro; IPR005639; endotoxin_N.
CC InterPro; IPR008979; Gal_bind_Like.
CC Pfam; PF03944; Endotoxin_C; 1.
CC Pfam; PF0555; Endotoxin_M; 1.
CC Pfam; PF03945; Endotoxin_N; 1.
CC Direct protein sequencing; Sporulation; Toxin.
CC SEQUENCE 1157 AA; 129775 MW; C364391EF7DFB8A CRC64;
CC
Qy Query Match 33.1%; Score 1127.5; DB 1; Length 1157;
Db Best Local Similarity 36.1%; Pred. No. 6.7e-65;
Qy Matches 250; Conservative 148; Mismatches 217; Indels 77; Gaps 19;
Qy 1 MNPNNRSHDTIKVTPNSELOTNEN-QYPLADNPNTLEELNYKEFLRWEDSSTEVLDN 59
Db 1 MNRNNQNEYIID-APHGCGFSDDDRYPLASDPNAAQLNMNYKDYQLQMTDEDYDYSIN 59
Qy 60 STV---KDAVGTGIVSVGVGQILGVVVPFAGALTSTFYQSFLNTIWP-SDADPWKAFMAQV 114
Db 60 PLSISGRDANVQTALTVVGRILGALGVFPQGIVSFYQFLNTLTPVNDTALWEAFMRQV 119
Qy 115 EVLIDKKIEYAKSALAELOGLQNNFEDYVNALNSWKKTPLSLRS-KRSQRIRELFQ 173
Db 120 EELVNNQITEFARNQALARLOGLGDSFNVYQKSLQNW---LADRNDTRNLSSVRAQFTA 175
Qy 174 AESHFRNSMPSFAVSKFEVLPLTYAQAANTHLLLLDKDAQVGEWGYSSDEVAEFYHRQ 233
Db 176 LLDLDFVNAIPLFVAVNQOQVPLLSVYAQAANLHLLLLDKDASLFGEGWGTQGEISTYYDRQ 235
Qy 234 LKLTQOYTDHCVMWYVGLNGLRGSTYDAWKFNFRREMTLVLDLVLFPFFYDIRLYS 293
Db 236 LELTKYNTYETWNTGLDRLRGNTESWLRYHQFRREMTLVLDVVALFPYDVLVLP 295
Qy 294 KGVKTELTRDIFTDPIF-----SLNTLOEYGP---TFLSIENS-IRKPHLFDYLOQIEF 343
Db 296 TGSNPQLTREYVTDPIVENPPANVGLCRRWGTNPYNTFSELENATIRPPLFDRLNSLTI 355
Qy 344 HTRLOPGYFGKDSFNVHSGNYVETRPISGSKTITSPFY-----GDKSTEPVQ 391
Db 356 SSNREF--VSSNFMIDWSGHTL--RRSYLNDLSAQQEDSYGLITTTTATINPGVDGNRIE 411
Qy 392 KLSFPGQKVYRTIANTDVAWPNKGKYLGVTKVDFSOYDDQKNETSTQTYDSKRNNGHV 451
Db 412 STAVDFRSGALIGYVNRASFPVGGFLNGTT-----SPANGGCRD 451
Qy 452 AQDSIDQLPPEPTTDEPLEKAYSHQNYAEACFLMDRR-----GTIFFTWTHRSVDFF 504
Db 452 LYDNTDELPPDBS---TGSSTHRLSHVTFEFQTNQAGSIANAGSVPTVYVTRRDVDLN 507
Qy 505 NTIDAETKITQLPVVKAYALSASGASIEGPGTGNLLFLKSSNSIAKPKYTLNSAALLQ 564
Db 508 NTITPNRITQPLVKASAPVSGTTLVKGPFGTGGGIL--RRITNGTFTGLURVTVNS-PLUQ 565
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CC -----
DR HSPB; L32020; AAA22344.1; -.
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
SQ SEQUENCE 1229 AA; 139769 MW; A4C949DB675C3269 CRC64;

Query Match 32.9%; Score 1122; DB 1; Length 1229;
Best Local Similarity 36.7%; Pred. No. 1.7e-64;
Matches 247; Conservative 126; Mismatches 248; Indels 52; Gaps 16;

QY 1 MNPNNRSEHDTIKVTPNSELOTHNQYPLADNPSTLEELNYKEFLRMTEDS----STEV 56
DB 1 MTSNRKNENEII-----NALSIPTVSNPST---QMNLSPDARI-EDSLCVAEVNN 46

QY 57 LONSTVKDVGTSISVVGQILGVGVPPFAGALTSPYQSFLNTIMPDSADPWKAFMAQVEV 116
DB IDPFVSASTVQGINAGRIAGLVGVPPFAGLASFYSLVGLWPSGRDPWEIFLEHVEQ 106

QY 117 LIDKTEEVAKSALAELOGLQNNFEDYVNALNSWKTPLSLRKSRQDRIRLEFSQAES 176
DB LIRQOQVTRNTARLEGLRGYRSYQOALETWLD---NRNDARSIIILERYVALEL 163

QY 177 HFRNSMPFAVSKFEVLFTPTAQAAANTHLLKDAQVFGEEWGSSEDAVFYHRQLKL 236
DB DITTAIPLRIRNEEVPLLMVYQAANLHLLLRDASLFGSEWGMASDVNQYQOIRY 223

QY 237 TQOYTDHCNVNWNGLRGSTYDAWKFNFRREMTITVLDLIVLPFFYDIRLYSKGV 296
DB TEEYSNHCQVQWYNTGLNNLRGTNAESWLRYNQPRDLTLGLVDLVALFPSTYDTRYPINT 283

QY 297 KTELTRDITFDPI-----PSLNTLOEYGTFTLSIENSI-RKPHLFDYLGQIEFHTR 346
DB SAQLTREIYTDPIGRTNAPSGFASTWNNNAPSFAIAEALFRPHLLDFFPEQLTIYS- 342

QY 347 LQPGYFGKDSFNWGSNGYVETRPISGSKTITSPFYCDKSTBPVQKLSFDGQKVRTIAN 406
DB ASSRWSSSTQHMNVYVGHRLNFRPIGGLTNTSTOGLTNTSINPV-TLQFTSRDVRVTESN 401

QY 407 TDVAAMPNGKYLGVTKVD-----FSQYDDQK-NETSTQYDSKRNKNGHVSAQDSIDQJ 459
DB A-----GTNILEFTTPVNGVPWAFENFINQNIYERGATTYSQPYQGVIGLQIFDSETEL 454

QY 460 PPETTDEPLEKAYSHOLNAYECFLMODRGTIPFFFTWTHRSVDFFNTIDAEKITQLPVVK 519
DB PPETTERPNYESHRLSHLIGLIIGNTLRA--PVSWTHRSADORTWIGNRITQILPVK 512

QY 520 AYALSSGASIIIEGPGFTGGNLLFLKBSNSSIAKFKVTLNSAALLQRYRIRYASTNNLR 579
DB ALNLHSGTVVGGPGFTGGDIL-RRNTGTGFGDIRLNN-VPLSRQYRVRIRYASTTDLQ 570

QY 580 LFVQNSNNDPLVIYINKTKMKDDLTYYOTFDLATNNSMGFGDKNELIIGAESFVSNEK 639
DB FFRINGTTNIGNFSRTNRGNLEYSRFTAGFTPTFPNFLNAQSTFTLGAOSP-SNOE 629

QY 640 IYDKIEFIPVOL 652
DB VIYDRVEFVPAEV 642
```

RESULT 14

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CLBC_BACTM STANDARD; PRT; 1233 AA.
ID CLBC_BACTM AC Q45774;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Peptidicidal crystal protein cryIbC (Insecticidal delta-endotoxin
DE CryIbC) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name=cryIbC; Synonyms=cryIb(C), cryIb;
OS Bacillus thuringiensis (subsp. morrisoni).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1441; [1]
RN SEQUENCE FROM N.A.
RP Bishop A.H., Bone E.J., Ellar D.J.;
RT "Cloning of novel Bacillus thuringiensis delta-endotoxin.";
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGES: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z46442; CRA86568.1; -.
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
SQ SEQUENCE 1233 AA; 140451 MW; 7318382413529F21 CRC64;

Query Match 32.9%; Score 1122; DB 1; Length 1233;
Best Local Similarity 36.7%; Pred. No. 1.7e-64;
Matches 247; Conservative 126; Mismatches 248; Indels 52; Gaps 16;

QY 1 MNPNNRSEHDTIKVTPNSELOTHNQYPLADNPSTLEELNYKEFLRMTEDS----STEV 56
DB 1 MTSNRKNENEII-----NALSIPTVSNPST---QMNLSPDARI-EDSLCVAEVNN 46

QY 57 LONSTVKDVGTSISVVGQILGVGVPPFAGALTSPYQSFLNTIMPDSADPWKAFMAQVEV 116
DB IDPFVSASTVQGINAGRIAGLVGVPPFAGLASFYSLVGLWPSGRDPWEIFLEHVEQ 106

QY 117 LIDKTEEVAKSALAELOGLQNNFEDYVNALNSWKTPLSLRKSRQDRIRLEFSQAES 176
DB LIRQOQVTRNTARLEGLRGYRSYQOALETWLD---NRNDARSIIILERYVALEL 163

QY 177 HFRNSMPFAVSKFEVLFTPTAQAAANTHLLKDAQVFGEEWGSSEDAVFYHRQLKL 236
DB DITTAIPLRIRNEEVPLLMVYQAANLHLLLRDASLFGSEWGMASDVNQYQOIRY 223

QY 237 TQOYTDHCNVNWNGLRGSTYDAWKFNFRREMTITVLDLIVLPFFYDIRLYSKGV 296
DB TEEYSNHCQVQWYNTGLNNLRGTNAESWLRYNQPRDLTLGLVDLVALFPSTYDTRYPINT 283

QY 297 KTELTRDITFDPI-----PSLNTLOEYGTFTLSIENSI-RKPHLFDYLGQIEFHTR 346
DB SAQLTREIYTDPIGRTNAPSGFASTWNNNAPSFAIAEALFRPHLLDFFPEQLTIYS- 342
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QY 347 LQPGYFGKDSFNWYSGNYVETRPISGSKTITSPFYGDKSTPEPVQKLSFDGQKVYRTIAN 406
D 343 ASSRWSSTQHMNVYVGHRLNFRPIGGTINTSTQGLTNTNSINPV-TLQFTSRDYRTESN 401
QY 407 TDVAANPQKYLIVGTQVD-----FSQYDDQK-NETSTQYDYSKRNGHVSQADSIDLQ 459
D 402 A-----GTNLTTPVGVPMARFNPQNIYERGATTSQPYQGVGQLFLPSETL 454
QY 460 PPETTDPLEKAYSHOLNVAECFLMQDRGTIPFTTWTHTSRVDFNTIDAETKLTOLPVVK 519
D 455 PPETTERPNVSYSHRUSHGLIIGNTLRA--PVYSWTHRSADRTNTIGNRITQIPLVK 512
QY 520 AYALSSGASIIIEGPGFTGGNLLFLKSSNSIAKFKVTLSAALQRYRVRIRVASTTNLR 579
D 513 ALNLHSGVTVVGGPGFTGGDIL-RRNTGTGFDIRLAIN-VPLSQRYRVRIRVASTIDLQ 570
QY 580 LFVQNSNDLFLVIYINKTMKODDLTYQTDPLATNNSMGFGSKNBLIIGASFVSNEK 639
D 571 FFRINGTTNIGNFSRTMRGDNLEYSRPTGFTSPFNFLNAQSTFTILCAQSF-SNOE 629
QY 640 IYIDKIEFIPVOL 652
D 630 VIIDRVSEFPAEV 642

RESULT 15
C1KA_BACTM STANDARD; PRT; 1215 AA.
AC Q45715;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-MAY-2000 (Rel. 39, Last sequence update)
DE Peptidicidal crystal protein cry1Ka (Insecticidal delta-endotoxin
DE Cry1K(a)) (Crystalline entomocidal protoxin) (137 kDa crystal protein).
GN Name=cry1Ka; Synonyms=cry1K, cry1K(a);
OS Bacillus thuringiensis (subsp. morrisoni).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1441;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FI90;
RX MEDLINE=96102856; PubMed=8586263; DOI=10.1016/0378-1097(95)00397-1;
RA Koo B.T., Park S.-H., Choi S.-K., Shin B.S., Kim J.I., Yu J.H.;
RT "Cloning of a novel crystal protein gene cry1K from Bacillus
RT thuringiensis subsp. morrisoni".
RL FEMS Microbiol. Lett. 134:159-164 (1995).
CC -1- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut
CC epithelial cells of insects. Selectively toxic to Artoidea rapae
CC but not active on Plutella xylostella.
CC -1- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -1- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -1- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
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DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
SQ SEQUENCE 1215 AA; 137378 MW; 7CAF7A3311893D9B CRC64;

Query Match 32.9%; Score 1121; DB 1; Length 1215;
Best Local Similarity 37.9%; Pred. No. 1.9e-64;
Matches 251; Conservative 126; Mismatches 247; Indels 38; Gaps 16;

QY 1 MNPENSEHDTIKVTNPSELQTNHNOYPLADNNSLTLEELNYKEFLRMSTDSSTEVLDNS 60
D 1 MNSNRKNENIINALSIPAVNSHAQMDL--SPDRIE-----DSCVAEGNN---IDPF 50
QY 61 TVKDAVGTGIVSVVQGLGVGVFPFAGALTFSYSELTNIWPSDADPWKAPMAOVVLI-D 119
D 51 VSASTVQTGSIAGRILGVLPFAGOLASFYSLVGLWPSGRDPWEIMEHVEQIVRQ 110
QY 120 KKEEVAKSKALAELOGLQNNFYVNALNSWKKTPLSLRKSRQDRIRLFSQAESHFR 179
D 111 QQTIDSVRDTAIARLEGLGRGYSYQQALETWLD---NRNDARSRSIIRERYIALELDIT 167
QY 180 NSMPSFAVSKFEFLPVTYAAANTHLLLLKDAQVGEEMGYSSYEDVAEYFHRQLKLTQ 239
D 168 TALPLFSIRNEEVPPLMWYAAANLHLLURDASLFGSEMGMSADVNYIQOIRITE 227
QY 240 YTDHCYNNVYVGLNGLRGSTYDAWKFNRRFRREMTLTVDLI1VLPFFYDIRLSKGVKTE 299
D 228 YSNHCYQVYNTGLNRLRGTTAETWRYNQFRRLDTLGLVDLVALFPSYDTRTPIPTAQ 287
QY 300 LTRDIDFTDPIFSL-----NTLQEVGPTFLSIENS-IRKPHLFDYLOGIEFHTRLQPVFGK 354
D 288 LTRVYTDPNVGVAGPNNSWFRNGASFSAIENAIIRQPHLYDFLTNLTIYTR--RSQVGT 345
QY 355 DSFNYSYGNVYVTRPSIGSSKTTITSPFYGDKSTPE--VQKLSFDGQKVYRTIAN 412
D 346 TINLWAGHRITNRIQGGG---TSENVGAINPVSVSDIPFNVRDVTIVTSIAGGLGS 402
QY 413 PNGKVLGVTKVDQFSQYDDQKNETSTQTYDSEKNNGH---VSAQDSIDOLPPTTDEPL 468
D 403 LSGIRY-GLTRVDVDMIRNHPDIVTGLF---YHPGHAGIATQVKDSDELPLETTQPN 458
QY 469 EKAYSHQNLNVAECFLMQDRRGITPFTTWTHTSRVDFNTIDAETKLTOLPVKVALSSGAS 528
D 459 YRAFPHLLSHIS--MGPTTQDVPVYSWTHQSADRTNINSDRITQIPLVKAHTLQSGTT 516
QY 529 IIEGPGFTGGNLLFLKSSNSIAKFKVTLSAALQRYRVRIRVASTTNLRFLVQNSND 588
D 517 VVKGPGFTGGDIL-RRTSGGPPAFSNVNDL-FNLQRYRARIYASTNRIYVTVAGER 574
QY 589 FLVIYINKTMKODDLTYQTDPLATNNSMGFGSKNBLIIGASFVSNEKIYIDKIEFI 648
D 575 IFAGQFDKTMADAGAPLTFQSFVATINTAFTFPERSSSLTIGADTFSSNGNEVVDREFELI 634
QY 649 PV 650
D 635 QV 636

RESULT 16
C7AA_BACTU STANDARD; PRT; 1138 AA.
ID C7AA_BACTU
AC Q03749;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cry7Aa (insecticidal delta-endotoxin
DE CryVIIA(a)) (Crystalline entomocidal protoxin) (129 kDa crystal
DE protein).
GN Name=cry7Aa; Synonyms=cryIIic, cryVIIA(a);
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
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RX MEDLINE=92384571; PubMed=1514800;
RA Lambert B. Hofte H., Anny K., Jansens S., Soetaert P., Peferoen M.;
RT "Novel Bacillus thuringiensis insecticidal crystal protein with a
RL silent activity against coleopterian larvae.";
CC -!- FUNCTION: Promotes colloidotomic lysis by binding to the midgut
CC epithelial cells of Coleoptera. This protein is not toxic in its
CC natural form. It is highly toxic to Colorado potato beetle larvae
CC after an in vitro solubilization and trypsin activation step.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M64478; AAA22351.1; -.
DR EMBL; A07236; CAA00646.1; -.
DR PIR; A48944; A48944.
DR HSSP; P07130; 1DLCL.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR Spoolation; Toxin.
DR KW SEQUENCE 1138 AA; 129391 MW; 69D8676D46A1FAC CRC64;
DR QY Query Match 32.9%; Score 1119; DB 1; Length 1138;
DR DB Best Local Similarity 36.8%; Pred. No. 2.4e-64;
DR M Matches 251; Conservative 120; Mismatches 237; Indels 74; Gaps 19;
DR QY 1 MNPNNRSEHTIKVTPNSELQTNHQVPLADNPNSTLEELNYKEFLRMTEDSSSTEVLDS 60
DR DB 1 MNLNLDGSDSNTLNLSL-----NYPTKALSPSLKMNWQDFLSIYERQPEALASG 55
DR QY 61 TVKDAVGTGIVSVGQIILGVGVFPFAGALTSFYQSLNTIWPSDADPWKAFMAQVEVLIDK 120
DR DB -AINTVSVTGATLSALGVGASFTITFYLIKAGLLWPENKGIWDEFMTEVEALIDQ 113
DR QY 121 KIEEYAKSKALAELOGLQNNFEDVYNALNSW---KKTPLSLRKRQDRIRLFSAESH 177
DR DB 114 KIEEYVKNKAETAEIDGLGSLADKYQKALADWLKGQDDPEAILSVATEFRI-----IDSL 167
DR QY 178 FRNSMPSFAVSKFVFLPTVYQAQANTHLLLLKDAQVGEWGYSSDVAEFYHRQLKT 237
DR DB 168 FEFMPSFGKVGIEPLITVYQAQANHLALRDLSTLYGKMGFTQNNIENYRQKRI 227
DR QY 238 QOYTDHCNNVYNGVGLRGSTYDAWVKFNRFRREMTLTVLDLVLPPFDIILYSGVKV 297
DR DB 228 SEYSDHCTKWNSGLSLRGSTYEQWVINYRFRREMTLMALDLVAVFPFDPDRRSMETS 287
DR QY 298 TELTRDITDIPFSLNTLOEGPTFLSTEN-SIRKPHLFYDLOGIEPHT-----RLQ 348
DR DB 288 TQLTREVTDDVSLISNPDIDGFSQSNENTALTPTPLHVDLYLDTYTSKYKAFSHEIQ 347
DR QY 349 PGYFGKDSFNWGSNGVYETRPSIGSKTITSPPFYGDKSTFVQK--LSFDGQKYRTIAN 406
DR DB 348 PDLF-----YSAHKVSFKS-EQSNLYTTGIYG-KTSGVISSGAYSFHGNDIYRTLAA 399
DR QY 407 TDVAAMPNGKYLGVTKVDFQYDQKNETQYDYSKRNNGHVSADSDIQLPPEPTTE 466
DR DB 400 PSVVVYPTQNY-GVEQVEFYGVKGVHVRGDNKYD-----LTYDSIDQLPDP--GE 448

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QY 467 PLEKAYSHOLNVACFLMOD---RRCTIFFTWTHTSRVDFENTIDAEKITOLPVPVKAYAL 523
DB 449 PIHEKYTHRLCHATAIFKSTPDYDNATIFISWTHRSABYIYNNRIYPNKTIKIPAVKMYKL 508
QY 524 SSASIIIEGPGFTGGNLLFLKSSNSIAKFKVTLNSAALLQRYVRIRYASTTNLFLVQ 583
DB 509 DDPSTVVGPGFTGGDLV-KRGSTGVIGIKATVNS-PLSQKYRVRYAT----- 557
QY 584 NSNDFLVYIN-----KTMKDDDLTYQTDFDLATTNSMGFSGDKNELIIG 630
DB 558 NVSGQENV-YINDKITLQTKFQNTVETIGEGKDLTYGSEFYIYESTIOPFDPHPKHTLH 616
QY 631 AESFVSNKIVYDKIFIPVOL 652
DB 617 LSDLSNNSSFYVDSIEFIPVDV 638

RESULT 17
ID Q9F0P8 PRELIMINARY; PRT; 719 AA.
AC Q9F0P8; 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CryII.
GN Name=cryII;
OS Bacillus thuringiensis.
OC Plasmid pBTC19.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BTC007; PubMed=12957903;
RX MEDLINE=22837682; PubMed=9.5207-5211.2003;
RA Song F., Zhang J., Gu A., Wu Y., Han L., He K., Chen Z., Yao J.,
RA Hu Y., Li G., Huang D.;
RA "Identification of cryII-type genes from Bacillus thuringiensis
RT strains and characterization of a novel cryII-type gene.";
RL Appl. Environ. Microbiol. 69:5207-5211(2003).
DR EMBL; AF211190; AAG43526.1; -.
DR HSSP; P02965; 1CIY.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR Plasmid.
DR KW SEQUENCE 719 AA; 81024 MW; 7E17481922C435E6 CRC64;
DR QY Query Match 32.8%; Score 1118.5; DB 2; Length 719;
DR DB Best Local Similarity 37.3%; Pred. No. 1.3e-64;
DR M Matches 253; Conservative 130; Mismatches 235; Indels 61; Gaps 17;
DR QY 1 MNPNNRSEHTIKVTPNSELQTNHQVPLADNPNSTLEELNYKEFLRMTEDSS 53
DR DB 1 MCLKNPDPKHQSLSNAKVKDKIATDS-----LKNETDIELKNINHDFLRSEHS 50
DR QY 54 TEVLNDSNTVKDAGTGISVVGQILGVGVFPFAGALTSFYQSLNTIWPSDADPWKAFMAQ 113
DB 51 ---IDPFVSASTIQTGIGIAGKILGTGVPFAGIASLYSFTLGBELPFGKGSQWEIFMEH 107
DR QY 114 VEVLIDKKIEEYAKSKALAELOGLQNNFEDVYNALNSW---KKTPLSLRKRQDRIRLF 173
DB 108 VEELIDQKISTYARNIALADLKGDLALAVYHESLESWK---NRRNARATSVVKSQYIA 164
DR QY 174 AESHPNPSMPSFAVSKFVFLPTVYQAQANTHLLLLKDAQVGEWGYSSDVAEFYHRQ 233

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Db 165 LELLFVQKPSFAVSGEVEPLLPYIAQAANLHLLLRDASVFGKEWGLSNQISQSTFFNRQ 224
Qy 234 LKLTQQYTDHCVMWYVGLNGLRGSTYDAVKNRFRRENTLTVDLIVLPFPYDRLYS 293
Db 225 VERTSDYSDHCWYKSYGLNGLRGSTYDAVKNRFRRENTLTVDLIVLPFPYDRLYS 284
Qy 294 KGVKTELTRIDFTDPIFSLNTLOEY-----GPTFLGIENS-IRKPHLFDYLOGIEF 343
Db 285 IKTSQTLREVYTDALCTVHPNASFASTTWNNAFSALESNAVRNPHLLDFLEQVTI 344
Qy 344 HTRLQPCYFQKDSFNWYVETRPISGSKTITSPPYGDKSTPPVQKLSFPGQKYRT 403
Db 345 YSLLS-RWSNTQYMNMGHRLFR-TIGGVLNTSTQGSTNTSINPV-TLPFTSRDYRT 401
Qy 404 IANTDVAAPNGKYLGVTKVDFSDQYDDQKNEISTQYDYSKRNNGHVA-----QDSIDLQ 459
Db 402 ESLAGLNLFTQPVN-GVPRVDF-----HWKPAFLPIASDNPYYLGVAGVGTQLODSENL 456
Qy 460 PPETDDEPLEKAYSHQNLNAYAECLFMQDRRGTPFFTWTHRSVDFPNTIDAEKITQLPVVK 519
Db 457 PPETGQPNYESYSHRLSHIGLISASHVKALV--YSWTHRSADRTNTEPNSITQPLVK 514
Qy 520 AYALSGASIIIEGPGFTGGNLLFLKSSNSIAKPKVTLSAALLQRYRVRIRYASTNLR 579
Db 515 AFNLSSGAAVRPGFTGGDIL-RRNTGTGFDIRVNIN-PPFAQRYRVRIRYASTTDLQ 572
Qy 580 LFVQ-----NSNNDFLVIYINKTKNKKDDLTQTPDLATNSNMGSGDKNELIAGES 633
Db 573 FHTSINKALNQG-----FSATMNRGEDLDYKTFRTVGTTPFGSDFQSTFTIGAWN 626
Qy 634 FVSNKEIYIDKIEFIPVOL 652
Db 627 FSSGNEVYIDRIEFVPEV 645

RESULT 18

C7AB_BACUC STANDARD; PRT; 1138 AA.
AC 045708;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Peptidicidal crystal protein cry7AB (Insecticidal delta-endotoxin
DE CryVIIa(b)) (Crystalline entomocidal protoxin) (130 kDa crystal
GN Name=cry7AB; Synonyms=cryVIIa(b);
OS Bacillus thuringiensis (subsp. *kumamotoensis*).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=132267;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD867;
RA Payne J.M., Fu J.M.;
RT "Coleopteran-active Bacillus thuringiensis isolates and genes encoding
RT coleopteran-active toxins";
RL Patent number US5286486, 15-FEB-1994.
CC -1- FUNCTION: Promotes colloidomotic lysis by binding to the midgut
CC epithelial cells of Coleoptera.
CC -1- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -1- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -1- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC EMBL: U04368; AAA21121.1; --
DR HSP: P07130; 1DLC.
DR InterPro: IPR001178; Endotoxin.
DR InterPro: IPR005638; endotoxin_C.
DR InterPro: IPR005639; endotoxin_N.
DR InterPro: IPR008979; Gal bind like.
DR Pfam: PF03944; Endotoxin_C; 1.
DR Pfam: PF00555; Endotoxin_M; 1.
DR Pfam: PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
SQ SSEQUENCE 1138 AA; 129658 MW; E12DC80COA56D1DA CRC64;

Query Match 32.8%; Score 1117; DB 1; Length 1138;
Best Local Similarity 37.2%; Pred. No. 3.2e-64;
Matches 253; Conservative 115; Mismatches 242; Indels 70; Gaps 19;

Qy 1 MNPNNRSEHDTIKVTNSELQTNHNOYPLADNPNTLEELNYKEFLRMTESSDEVLDNS 60
Db 1 MLNLNLGGYEDSNRTLNLSL-----NYPQKALSPSLKNMNYQDFLSITEREQPEALASG 55
Qy 61 TVKDAVGTGISVVGQILGVVGPFPAGALTSPFYQSFLNTIWPSDADPKAFMAQVEVLIDK 120
Db 56 NT--AINTVSVVTGATLSALGVFGASFITNFKITGLLWPHDKNTWDEFMTEVETLIEQ 113
Qy 121 KIEYAKSKALAELOGLQNNFEDYVVALNSWKTPLSRSKRSQDRIRELFSQAESHFRN 180
Db 114 KIEQYARNKALAELEGNNLTYYQALDELWNP---DDPATITRVIDRFRILDALFES 170
Qy 181 SMPFAVSKFEVLFLPTAQAANTHLLKDAQVFGSEMGYSSEDAEFYHRLKLTQQY 240
Db 171 YNPSRVAQVEIPLLTVAQAANLHLLLRDASVFGKEWGLSNQISQSTFFNRQ 230
Qy 241 TDHCVMWYVGLNGLRGSTYDAVKNRFRRENTLTVDLIVLPFPYDRLYSKGVKTEL 300
Db 231 SNHCVMWYVGLNGLRGSTYDAVKNRFRRENTLTVDLIVLPFPYDRLYSKGVKTEL 290
Qy 301 TRDIFTDPIFSLNTLOEYGTFFLSIEN-SIRKPHLFDYLOGIEFHT-----RLQPGY 351
Db 291 TREVTDPISLSISNPGISFQSOMENTAIRTHLDVLDLYIYSKYKAFSHEIQPDL 350
Qy 352 FGKDSFNWYVETRPISGSKTITSPPYGDKSTPPVQK--LSFDGQKYRTIANTDV 409
Db 351 F-----YNSAHKVPKQS-EQSNLYTTGIYG-KTSGYSSGAYSPRGNDIYRTLAAPSV 402
Qy 410 AAWPNKGYLVTKVDFSDQYDDQKNETSTQYDYSKRNNGHVAQDSIDQLPPTTDEPLE 469
Db 403 VVYPTQNTY-GVEQVEFYGVKGHVHVRGDNKYD-----LTYDSIDQLPPD--GSEPIH 451
Qy 470 KAYSHOLNVAECFLMQD--RRGTIPFFTWTHRSVDFPNTIDAEKITQLPVKAYALSSG 526
Db 452 EKXTHRLCHATAISKSTPDYDNATIPFSWTHRSAYRYRIYENKITKIPAVKMYKLGDT 511
Qy 527 ASIIEGPGFTGGNLLFLKSSNS-IAKPKVTLSAALLQRYRVRIRYASTNLRFLVQNS 585
Db 512 STVWKGPGFTGGDL--VKGSGNGYIGDIKATVNS-PLSQNYRVRVRYAT-----NV 559
Qy 586 NNDFLVIYN-----KTNKKDDLTQYTFDLATNSNMGSGDKNELIAGAE 632
Db 560 SQGFNY-YINDKITLQRKFQNTVETIGEGKDLTYGSGFYIEYSTTITQFPDKPKITLHLS 618
Qy 633 SFVSNKEIYIDKIEFIPVOL 652
Db 619 DLSNNSFFVDSIEFIPVDV 638

RESULT 19
CLID_BACTU STANDARD; PRT; 719 AA.
AC Q9XDL1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Pesticidal crystal protein cryIIId (Insecticidal delta-endotoxin)
DE CryII(d) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
GN Name=cryIIId; Synonyms=cryII(d), NRcryV;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BR30;
RA MEDLINE=20374042; PubMed=10919402;
RX Choi S.-K., Shin B.-S., Kong E.-M., Rho H.M., Park S.-H.;
RT "Cloning of a new Bacillus thuringiensis cryII-type crystal protein
gene.";
RL Curr. Microbiol. 41:65-69(2000).
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of many lepidopteran larvae. Active on Plutella
CC xylostella and on Bombyx mori.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC
CC EMBL; AF047579; AD44366.1; -.
DR HSSP; P02965; 1C1Y.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_Like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
SQ SEQUENCE 719 AA; 81403 MW; F335F5689D3B0C45 CRC64;

Query Match 32.8%; Score 1115.5; DB 1; Length 719;
Best Local Similarity 37.8%; Pred. No. 2.1e-64;
Matches 253; Conservative 123; Mismatches 225; Indels 69; Gaps 18;

QY 23 NHNQY-----PLADNPSTLEELNYKEFLRMTEDSSTE-VLDNSTVKDAV 66
DB 5 NQNWYRFSFNATVDKSFDTDPLEHNTNMEQLQNSNHEDECLKMSYESVEPFVSVTIQ--- 61

QY 67 GTGISVVGQILGVVGFAGALTSFYQSFLNTWPSDADPWKAFMAQVEVLDDKIEEYA 126
DB 62 -TGIGIAGKILGNLGVFFAGQVASYLSFILGELWPKGSKQWELFMHEVLELNQKISTYA 120

QY 127 KSAIAELQGLQNPEDYNALNWKPTPLSLKESQDRIRL-----FSQAESHPNSM 182
DB 121 RNKALADLKLGLDALAVYHESLESWE-----NRNTRVRSVKNQVIALELMFVQKL 173

QY 183 PPSAVSKFEVLFLPTAQANATHLLIKDAQVGEWGYSSSDVAFYHRLQKLTOQYTD 242
DB 174 PPSAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSESEISFYNRQSQTQEYSD 233

QY 243 HCWNVTNVLNGLRGSTYDAWVFNFRREMTLTVLDLVLFPFYDIRLSKGVKTELTR 302
DB 234 YCSEWYNTGLNRLGRNAESWVRNQPRDMTLWLDLVALFPSTYDTRMYPITPSAQLR 293

QY 303 DIFTDPIFSLNTLOEY-----GPTFLSIENS-IRKPHLDYLGQIEFFHRLQPGYF 352
DB 294 EYVTDALGTVHPNASFSTWYNNAPSFSTIEAAVRNPHLLDFLEQVITYLSLS-RWS 352

QY 353 GKDSFNWMSNGYVETRPISGSKSTITSPPFYGDKSTBPVQKLSFDGQKVRRTIANTVAW 412

DB 353 NTQYMNMGHGKLEFR-TIGTLNLTSTQGSTNTSINPV-TLPFTSRDVYRTESLAGLNLF 410
QY 413 PNGKVLGVTKVDFSQYDDOKNETSTQTYDSKRNHG-----VSAQDSIDOLPPTTDEPL 468
DB 411 LTQFVN-GVPRVDF-----HWKFVTHPIASNFYYPGYAGIGTQLQDSENELPPTTQPN 465
QY 469 EKAYSHOLNVAECFLMQDRRGTIPTFFTWTHRSVDFNTIDAETITQLPVVKAYALSSGAS 528
DB 466 YESYSHRLSHIGLISASHVALV--YSWTHRSADRTNTINSDSITQPLVKAFNLPSGAS 523
QY 529 IIEGPGFTGGNLLFLKSSNSIAKFKVTLNSAALLQRYVRIRYASTTNRLRFVQ----- 583
DB 524 VWRGPGFTGGDIL-QRTNTGTGDIRVNIN-PFPAQRYRLRIRYASTTNLEFFHTSINGKA 581
QY 584 -NSNDFLVIYINKTKNDDDLTYQTDFLATTSNMGFSGDKNELLIIGASFSVNEKIYI 642
DB 582 INQGN-----FSATMNRGEBLDYKAPRTVGTTPFSPFSAQSTFTTGAMNFSLGNEVIYI 635
QY 643 DKIEFIPVOL 652
DB 636 DRIEFVPEV 645

RESULT 20
C7AB_BACUA STANDARD; PRT; 1138 AA.
ID_C7AB_BACUA STANDARD; PRT; 1138 AA.
AC Q45707; 2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cry7Ab (Insecticidal delta-endotoxin
DE CryVIIA(b)) (Crystalline entomocidal protoxin) (130 kDa crystal
DE protein).
GN Name=cry7Ab; Synonyms=cryVIIA(b);
OS Bacillus thuringiensis (subsp. dakota).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=132268;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD511;
RA Payne J.M., Fu J.M.;
RT "Coleopteran-active toxins";
RT coleopteran-active toxins";
RL Patent number US5286486, 15-FEB-1994.
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of Coleoptera.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U04367; AAA21120.1; -.
DR HSSP; P07130; 1DLC.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_Like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
SQ SEQUENCE 1138 AA; 129778 MW; 01DF7072C074CE88 CRC64;

Query Match 32.6%; Score 1112; DB 1; Length 1138;
 Best Local Similarity 36.8%; Pred. No. 6.8e-64;
 Matches 248; Conservative 124; Mismatches 244; Indels 58; Gaps 19;

QY 1 MNPNNREHDITKVTNPSELQTNHNPPLADNPNTSTLEELNYKEFLRWEDSSSTEVLVNS 60
 DB 1 MNLNLLGGYEDSNRLNLSL-----NYPTQKALSPSLKNMNYQDFLSITEREQPEALASG 55

QY 61 TVKDAVGTGIVSGQILGCVGPAGALTSFYQSFPLNTIMPSDADPKAFMAQVEVLIDK 120
 DB 56 NT--AINTVSVTGATLSALGVPAGSFITNFKITGLWPHNKNINWDEFWTEVETLIEQ 113

QY 121 KIEEYAKSKALAEQLQGNPFEDVYNALNSMKTTPLSLRKSRQDRIRELFSQAEHFRN 180
 DB 114 KIEQYARNKALAELEGLGNLTIYQQALEDWLNPP---DDPATITRVIDRFRIILDALFES 170

QY 181 SMPFSAVSKFEVLPLPYTAQANHTLLLLKDAQVFGSEWGSVDVAEFVHRQKLTQQY 240
 DB 171 YMPFSRVAGYEIPLLTYYAQAANHLALLRDLSTLYGDKWGTQNNIEENTNRQKKHISEY 230

QY 241 TDHCVNMYNGLNGRSTYDAWKENREREMTLTVLDLVLFPFVDIRLYSKGVKTEL 300
 DB 231 SNHCVKYNGSLRANGSTIEQWYNRFRREMILMVDIAAVPPIYDPRMYSMETSTQL 290

QY 301 TRDIFTPIFSLNTLOEYPTFLSIEN-SIRKPHLFDYLOQIEPHT-----RLQPGY 351
 DB 291 TREVYTDPISLISNPIDIGSFSQMENTAFRPHLDVYLDLYYTSKYKAFSHEIQPDL 350

QY 352 FGKDSFNYWNGVNYETRPSIGSSKTTISPPYGDKSTFVQK--LSFGQKQYRTIANTDV 409
 DB 351 F-----YWCVHKVSPFKS-EQSNLYTTGIY-KTSGYISGAYSPRGNDIYRTLAAPSV 402

QY 410 AAMPNGKVLGVTKVDFSDYDQKNETSTQTYDSKRNNGHVSAQDSIDQLPPTTDEPLE 469
 DB 403 VVPYPTQNY-GVEQVEFYGVKGVHXYRGDNKYD-----LTYDSDQLPDP--GSPIH 451

QY 470 KAYSHQLNLYACEFLMQD---RRGTPEFTTHRSVDFPNTIDAEKITQLPWPVKAYALSSG 526
 DB 452 EKYTHRLCHATAISKSTPDYDNATIPFSTHRSAYEYNYRPNKIKKIIPAVKXKLDL 511

QY 527 ASIEGPGFTGNNLLFLKESNS-IAFKVTVLNSAALLQYRVIRVASTTN--LRLFVQ 583
 DB 512 STVVGFGFTGGDL--VKRSGNGYIGDIKATVNS-PLSKYKRVVRVATVSGLENVFI- 567

QY 584 NSNNDPLVIYN-----KTWNKDDLLTYQTFDLATNSNGFSGDKNELIIGAESFVNS 638
 DB 568 ---NDEIALQKQFQSTVETIGEGKDLTYGFGVIEYSTTIOFPNEHPKITLHLNLSNNS 624

QY 639 KIYIDKIEFIPVQL 652
 DB 625 PFYVDSIEFIPVDV 638

RESULT 21
 C11A BACTK
 ID C11A BACTK STANDARD: PRT: 719 AA.
 AC Q457E2; P71092; Q45750; Q45751; Q45756;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DE Pesticidal crystal protein cryIIa (insecticidal delta-endotoxin
 DE CryII(a)) (crystalline entomocidal protoxin) (81 kDa crystal protein).
 GN Names: cryIIa; Synonyms: CGCryV, cryII(a), cryV, cryV1,
 OS Bacillus thuringiensis (subsp. kurstaki).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=29339;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSIR732;
 RX MEDLINE=93298009; PubMed=8517758;
 RA Gleave A.P., Williams R., Hedges R.J.;
 RT "Screening by polymerase chain reaction of Bacillus thuringiensis

serotypes for the presence of cryV-like insecticidal protein genes and characterization of a cryV gene cloned from B. thuringiensis subsp. kurstaki.";
 Appl. Environ. Microbiol. 59:1683-1687(1993).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JHCC4835;
 RX MEDLINE=92269582; PubMed=1588820;
 RA Taylor R., Tippet J., Gibb G., Pells S., Pike D., Jordan L., Ely S.;
 RT "Identification and characterization of a novel Bacillus thuringiensis delta-endotoxin entomocidal to coleopteran and lepidopteran larvae.";
 Mol. Microbiol. 6:1211-1217(1992).
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HD-1;
 RX MEDLINE=95314293; PubMed=7793960;
 RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.-T., Lee S.-T., Kim J.-I.;
 RT "Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis and cloning of cryV-type genes from Bacillus thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp. entomocidus";
 Appl. Environ. Microbiol. 61:2402-2407(1995).
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB88;
 RX MEDLINE=96178985; PubMed=8606196;
 RA Kostichka K., Warren G.W., Mullins M., Mullins A.D., Palekar N.V., Craig J.A., Kozel M.G., Estruch J.J.;
 RT "Cloning of a cryV-type insecticidal protein gene from Bacillus thuringiensis: the cryV-encoded protein is expressed early in stationary phase";
 J. Bacteriol. 178:2141-2144(1996).
 [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=61;
 RA Selvapandian A., Bhatnagar R.K.;
 RT "Isolation, cloning and expression of cryV gene";
 Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 CC -I- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut epithelial cells of certain coleopteran and lepidopteran species.
 CC Active on Plutella xylostella and Bombyx mori.
 CC -I- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.
 CC -I- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.
 CC -I- SIMILARITY: Belongs to the delta endotoxin family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 DR EMBL; M98544; AAA22354.1; -;
 DR EMBL; X62821; CAA44633.1; -;
 DR EMBL; L36338; AAC36999.1; -;
 DR EMBL; L49391; AAB00958.1; -;
 DR EMBL; Y08920; CAA70124.1; -;
 DR PIR; I39815; I39815.
 DR PIR; S25383; S25383.
 DR HSSP; P02965; IC1Y.
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005638; endotoxin_C.
 DR InterPro; IPR005639; endotoxin_N.
 DR InterPro; IPR008979; Gal bind like.
 DR Pfam; PF03944; Endotoxin_C; 1.
 DR Pfam; PF00555; Endotoxin_M; 1.
 DR Pfam; PF03945; Endotoxin_N; 1.
 DR Sporulation; Toxin.
 FT VARIANT 159 159 K -> R (in strain 61).

05-JUN-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CryI.

GN Name=cryI;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
[1]

RP SEQUENCE FROM N.A.
RA Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY262167; AAP86782.1; ...
DR GO: 0005102; Fireceptor binding; IEA.
DR GO: 0006952; P:defense response; IEA.
DR GO: 0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAFF5 CRC64;

Query Match 32.3%; Score 1100.5; DB 2; Length 719;
Best Local Similarity 36.6%; Pred. No. 28-63;
Matches 249; Conservative 137; Mismatches 231; Indels 63; Gaps 19;

QY 1 MNPNNRSEHDTI-----KVTNSELQNNHNYPLADNPSTLEELANKYKFLRMTESS 53
DB 1 MKLNQDKHQSFSSNAKVDKISTDS-----LKNETDIELQNIHEDCLKMSYEN 50

QY 54 TE-VLDNSTVKDAVGTGIVGQILGVGVPPAGALTSTFYQSFLNTIWPSDADPWKAFMA 112
DB 51 VEPFVSASTIQ----TGIGIAGKILGTGVPPAGQVASYLSFILGELPKGNQWEIEME 106

QY 113 QVEVLIDKKIEYAKSALAELOGLQNNPFDYVNALNSWKTPPLSLRSKRQDRIELFS 172
DB 107 HVEEIIINQKISTYARNKALTDLKGLDALAVYHDSLESVWG---NRNNTARSVVKSYI 163

QY 173 QAESHFRNMPSPFASKPEVLPLPTVQAQANTHLLLDKDAQVGEWGYSSDEVAEFYHR 232
DB 164 ALELMFVQKLPSFASVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSEISTFYNR 223

QY 233 QLKLTQOYTDHCVMYVNLGLRGSTYDAWKENFRREMTLTVLVDLIVLFPFVDIRLY 292
DB 224 QVERAGDYSCHVKWYSTGLNLRGTNAESWRYNQFRDMTLMVLDLVALFPFSDYQMY 283

QY 293 SKGVKTELTRDIFTD-----PIFSLNT-LQEGPTFLSIENS-IRKPHLFDYLOGIE 342
DB 284 PIKTTAQLTREVVYTDAGTGVHPHPSFTSTTWNNAAPSFALEAAVVRNPHLLDFLEQVT 343

QY 343 FHTRLQPGYFGKDSFNWYSGNVVETRPISGSKTITSPFYGDKSTEPVQKLSFDGQKYR 402
DB 344 IYSLLS-RWSNTQYNNMGHKLFR-TIGGMLNTSTQGSTNTSINPV-TLPFTSRDVR 400

QY 403 TIANTDVAAPNGKVLGVTKVDFSOYDDQKNETSTQYDSCRNGH----VSAQDSIDQ 458
DB 401 TESLAGNLFLTPQVN-GVPRVDF----HWKVTHTPIASDNFFYPGYAGIGTQLQDSNE 455

QY 459 LPPETTDPELEKAYSHQLNYACFLMQDRRGITPFTTWTTHRSVDFNTIDAETITQLPV 518
DB 456 LPPEATGQPNYESYSHRLSHIGLSASHVKALV--YSWTHRSADRTNTIEPNSITQPLV 513

QY 519 KAYALSSGASIIEGPQGTGCLNLLFKESNSIAKPKVTLSAALLQRYVRIRVASTNL 578
DB 514 KAFNLSSGAAVRGPGFTGGDL-RTNTGTGFDIRVNIN-PPEAQRYVRIRVASTTDL 571

QY 579 RLPVQ-----NSNDFLVIYINKTNKDDLTCTYCTEDLATNNSMGSGDKNELIIGAE 632
DB 572 QPHTSINGKAIQGN-----FSATNKGEDLDYKTFRTVGTFTFPFSLDVQSTFTTGA 625

05-JUN-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CryI.

GN Name=cryI;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
[1]

RP SEQUENCE FROM N.A.
RA Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY262167; AAP86782.1; ...
DR GO: 0005102; Fireceptor binding; IEA.
DR GO: 0006952; P:defense response; IEA.
DR GO: 0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAFF5 CRC64;

Query Match 32.3%; Score 1100.5; DB 2; Length 719;
Best Local Similarity 36.6%; Pred. No. 28-63;
Matches 249; Conservative 137; Mismatches 231; Indels 63; Gaps 19;

QY 1 MNPNNRSEHDTI-----KVTNSELQNNHNYPLADNPSTLEELANKYKFLRMTESS 53
DB 1 MKLNQDKHQSFSSNAKVDKISTDS-----LKNETDIELQNIHEDCLKMSYEN 50

QY 54 TE-VLDNSTVKDAVGTGIVGQILGVVGPAGALTSFYQSFLNTIWPSDADPWKAFMA 112
DB 51 VEPFVSASTIQ----TGIGIAGKILGTGVPGQVASLYSFLGELAPKGNQWEIEME 106

QY 113 QVEVLIDKKIEYAKSALAELOGLQNNPFDYVNALNSWKTPPLSLRSKRQDRIELFS 172
DB 107 HVEEIIINQKISTYARNKALTDLKGLDALAVYHDSLESVWG---NRNNTARSVVKSYI 163

QY 173 QAESHFRNMPSPFVSKPEVLPLPTVQAQANTHLLLDKDAQVGEWGYSSDEVAEFYHR 232
DB 164 ALELMFVQKLPSFVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSEISTFYNR 223

QY 233 QLKLTQQYTDHCVNMYNGLNGRSTYDAWKENFRREMTLTVDLILVFPFVDIRLY 292
DB 224 QVERAGDYSCHVKWYSTGLNLRGTNAESWRYNQFRDMTLMVLDLVALFPSTQMY 283

QY 293 SKGVKTELTRDIFTD-----PIFSLNT-LQEGPTFLSIENS-IRKPHLFDYLOGIE 342
DB 284 PIKTTAQLTRVYVTDAGTGVHPHPSFTSTTWNNAAPSFALEAAVVRNPHLLDFLEQVT 343

QY 343 FHTRLQPGYFGKDSFNWYSGNVVETRPISGSKTITSPFYGDKSTEPVQKLSFDGQKYR 402
DB 344 IYSLUS-RWSNTQYNNMGHKLFR-TIGGTLNISTQGSTNTSINPV-TLPFTSRDVR 400

QY 403 TIANTDVAAPNGKVLGVTKVDFSOYDDQKNETSTQYDSCRNGH----VSAQDSIDQ 458
DB 401 TESLAGNLFLTPQVN-GVPRVDF----HWKVTHTPIASDNFYPGYAGIGTQLQDSNE 455

QY 459 LPPETTDPELEKAYSHQLNYACFLMQDRRGITIPFTWTHRSVDFNTIDAETITQLPV 518
DB 456 LPPEATGQPNYESYSHRLSHIGLISASHVKALV--YSWTHRSADRTNTIEPNSITQPLV 513

QY 519 KAYALSSGASIIEGPQGTGCLNLFKESNSIAKPKVTLSAALLQRYVRIRVASTNL 578
DB 514 KAFNLSSGAAVRGPGFTGGDL-RTNTGTGFDIRVNIN-PPEAQRYVRIRVASTTDL 571

QY 579 RLPVQ-----NSNDFLVIYINKTNKDDLTCTYCTEDLATNNSMGSGDKNELIIGAE 632
DB 572 QPHTSINGKAIQGN-----FSATNRGEDLDYKTRVGTFTFPFSLDVQSTFTTGAW 625

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Db 456 LPPEQTGPVYESYSHRLSHIGLISASHVKALV--YSWTHRSADRTNTIEPNSITQIPLV 513
QY 519 KAYALSSGASIIIEGPGFTGGNLLFLKESNSAKFKVTLNSAALLQVRVRIRYASTTNL 578
Db 514 KAFNLSSGAAYVRGPGFTGGDIL-RRNTGTGDIRVNIN-PPFAQRYVRIRYASTTDDI 571
QY 579 RLFVQ-----NSNDFLVIYINKMKDDDLTYOTFDLATNNSMGFGSGDKNELIIGAE 632
Db 572 QFHTSINGKAINQGN-----FSATMNRGEDLDYKTFRTVGTFTTFFSFDVQSTTIGAW 625
QY 633 SFVSNKIIYIDKIEFIPVOL 652
Db 626 NFSSGNEVYIDRIEFVPEV 645

RESULT 25
085796 PRELIMINARY; PRT; 719 AA.
AC O85796;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Insecticidal protein.
GN Name=crv101;
OS Bacillus thuringiensis (subsp. kurstaki).
OG Plasmid large plasmid.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8101;
RA Zhong Q., Long Q., Yuan M., Pang Y., Wang X.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF076953; AAC26910.1; -.
DR HSSP; P02965; 1CIY.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0003405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR Plasmid.
SQ SEQUENCE 719 AA; 81230 MW; 42746D478359BBA7 CRC64;

Query Match 32.1%; Score 1094.5; DB 2; Length 719;
Best Local Similarity 36.5%; Pred. No. 5e-63;
Matches 248; Conservative 137; Mismatches 232; Indels 63; Gaps 19;

QY 1 MNPNNRSEHTI-----KVTNSELQNNHNOYPLADNPNSTLEELNYKEFLRMTEDSS 53
Db 1 MRLKNQDKHQSFSSNAKVKDISTDS-----LKNETDIELQNHEDCLKMSEYEN 50
QY 54 TE-VLDNSTVKAVGTCISVGGQILGVGPYPAGALTSEYQSFNLTIWPSDADPWKAFA 112
Db 51 VEPFVSASTIQ----TGIGIAGKILGTGLVPAGQVASIYSFILGLWPNGKNQWEIFME 106
QY 113 QVEVLIDKIEEYAKSAELAEQLQGNFEDYVNALNSWKTKPLSLRSKRSDRIELFSL 172
Db 107 HVEEIIINQKISTYARKNALTDLKGLDALAVHDSLESVVG---NENNTARSVVKSQYI 163
QY 173 QAESHPRNMPSPAVSKFEVLFLPTVAQANTHLLLLKDAQVFGEBWGSDDVAEFYR 232
Db 164 ALELMFVQKLPSPAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNR 223
QY 233 OLKLTQOYTDHCYNNVNGLGRGSTYDAWVKFNEFRREMTITVLDDLVLPPFYDIRLY 292
Db 224 QVERAGDYSDBCHVKWYSTGLNNIRGNAESWRYNGFRDMLTLMVLJLVALFPSTQMY 283
QY 293 SKGVKTELTRIDFTD-----PIFSLNT-LQEYGFTEFLSIENS-IRKPHLFDYLOGIE 342
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Db 284 PIKTTAQLTREVVYDAIGTVHPSPSTTWNYNAPSFAIEAAVVRNPHLLDFLEQVT 343
QY 343 FHTLQPGYFGKDSFNWWSGNYVETRPSIGSSKTIITSPFYGDKSTERPQKLSFDGQKYR 402
Db 344 IYSLLS-RWSNTQTMNMMWGGHKLFR-TIGTGLNISTQGSTNTINPV-TLPFTSRDYR 400
QY 403 TIANTDVAAMPNGKYYILGVTKVDFSQYDDQDNKSTSTQYDSKRNGH----VSAQDSIDQ 458
Db 401 TESLAGLNLFTQPN-GVPRVDF----HWKFVTHPIASDNFYPGYAGITQLQDSENE 455
QY 459 LPPETTDPELEKAYSHQINAYAECLFMQDRRTGTFPFTWTHRSVDFEFTIDAEKTLQLPV 518
Db 456 LPPEATGPVYESYSHRLSHIGLISASHVKALV--YSWTHRSADRTNTIEPNSITQIPLV 513
QY 519 KAYALSSGASIIIEGPGFTGGNLLFLKESNSIAKFKVTLNSAALLQVRVRIRYASTTNL 578
Db 514 KAFNLSSGAAYVRGPGFTGGDIL-RRNTGTGDIRVNI-KPPFAQRYVRIRYASTTDL 571
QY 579 RLFVQ-----NSNDFLVIYINKMKDDDLTYOTFDLATNNSMGFGSGDKNELIIGAE 632
Db 572 QFHTSINGKAINQGN-----FSATMNRGEDLDYKTFRTVGTFTTFFSFDVQSTTIGAW 625
QY 633 SFVSNKIIYIDKIEFIPVOL 652
Db 626 NFSSGNEVYIDRIEFVPEV 645

RESULT 26
C1BA_BACTK STANDARD; PRT; 1228 AA.
AC P05517; O45731;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIIa (insecticidal delta-endotoxin
DE CryIIa(a)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name=cryIIa; Synonyms=cryA4, cryIIa(a);
OS Bacillus thuringiensis (subsp. kurstaki), and
OS Bacillus thuringiensis (subsp. entomocidus)
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339, 1436;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=HD-2;
RX MEDLINE=88203216; PubMed=3362680;
RA Brizzard B.L., Whiteley H.R.;
RT "Nucleotide sequence of an additional crystal protein gene cloned from
RT Bacillus thuringiensis subsp. thuringiensis.";
RL Nucleic Acids Res. 16:2723-2723(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.entomocidus; STRAIN=HD-110;
RA Soetaert P.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X06711; CAA29898.1; -.
```

```
DR EMBL; X95704; CAA65003.1; -.
DR PIR; S00873; S00873.
DR HSP; P07130; 1DLC.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
FT VARIANT 150 150 Y->H (in strain HD-110).
SQ SEQUENCE 1228 AA; 139647 MW; C8E3A19F5D98575 CRC64;

Query Match 31.5%; Score 1072.5; DB 1; Length 1228;
Best Local Similarity 36.6%; Pred. No. 2.9e-61;
Matches 246; Conservative 120; Mismatches 247; Indels 59; Gaps 19;

QY 1 MNPNNRSEHDTIKVTPNSELQTNHNOYPLADNPNTLLEELNYKEFLRMTDSSTEVLDNS 60
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1 MTSNRKNEEIIINAVNSHAQMD-----LLPDARIEDSLCIAEGNN--IDPF 45

QY 61 TVKDAGTGVSVGGIILGVGVPPAGALTSFYQSFLNTIWPSDADPKMAQVEVLIDK 120
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
46 VSASTVQTGINIAGRIILGVLPFAGQLASFYSLVGEIWPGRDQWEI FLEHVEQLNQ 105

QY 121 KIBEYAKSKALAELOQNNFEDYVNALNSWKKTPLSLRSKRQDRIRE-LFSQ---AES 176
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
106 QITENARNTALARLOGLGDSFRAYQOSLEDWLE-----NRDARTSVLYTYQYIALEL 158

QY 177 HFRNSMPSFAVSKFEVLFLPTYAQAANTHLLLLKDAQVGEEGYSESDVAEYFHRQLK 236
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
159 DFLNAMPFAIRNOEYVPLLMVYQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVER 218

QY 237 TQOYTDHCYVNVYVGLNGLSYDAWKFNRRERMTLVLDLVLFPYDRLVSKGV 296
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
219 TRDYSYCVIEWNTGLNSLRGTNAASWVRYNQRRDLTLGLVDLVALFPYSYDTRTYPI 278

QY 297 KTELTRDIFTDPI-----FSLNTLQOYGPFTLSIE-NSIRKPHLPDYLOGIEFHTRLQ 348
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
279 SAQLTREVTYDAIGATGVNMAWNNVNNAPSFAIEAAAIRSPHLLDPLEQITIFS-AS 337

QY 349 PGYFGKDSFNYSNGVYETRPSIGSSKTIITSPYQ--DKSTEPVKQLSPDGQKYRTIAN 406
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
338 SRWSNTRHMYWRGHTIQSRPIGGGLTST--HGATNTSINPV-TLRFASRDVYRTESY 393

QY 407 TDVAAMPNGKYL----GVTKVDFSQYDDQK-NETSTQTYDSCRNGHVSQAQSIDQLPP 461
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
394 AGVLLM---GIYLEPIHGVTFRFNTNPQNISDRGTANYSQPYESFGLQKDSLETLP 450

QY 462 ETTDEPLEKAYSHQLNVAECFLMQDRGTIPFTTWRHSVDFNTIDA EKITQLPVVKAY 521
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
451 ETTERPNYESYSHRLSHIGILOS--RVNVPVSWTHRSADRNTIGPNRITQIPVKAS 508

QY 522 ALSGASIIPEGPGFTGNLLFLKESNSIAKFKVTLSAALLQRYRIRYASTTNLRLF 581
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
509 ELPGQTTVVRGPGFTGGDIL-RRNTGCGPIRVTVN-GPLTQRYRIGFYASTVDPDF 566

QY 582 VQNSN---NDELVIYINKTKNKKDDLTQYTFDLATNNSMGFGSGDKNELIIGAESFVNE 638
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
567 VSRGGTTVNNFRFL---RTWNSGDELKYNFVRAFTTPTFTQIQDIIRTSIQGLSGNG 623

QY 639 KIYDKIEPIPV 650
DB 624 EVYDKIEPIPV 635
```

RESULT 27

Q93NM5

ID Q93NM5

AC Q93NM5;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

```
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CrylBa.
GN Names: crylBa;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang J., Song F., Huang D.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF368257; AAK63251.1; -.
DR HSP; P07130; 1DLC.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1228 AA; 139665 MW; E86D9842341FB439 CRC64;

Query Match 31.5%; Score 1071.5; DB 2; Length 1228;
Best Local Similarity 36.6%; Pred. No. 3.4e-61;
Matches 246; Conservative 119; Mismatches 248; Indels 59; Gaps 19;

QY 1 MNPNNRSEHDTIKVTPNSELQTNHNOYPLADNPNTLLEELNYKEFLRMTDSSTEVLDNS 60
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1 MTSNRKNEEIIINAVNSHAQMD-----LLPDARIEDSLCIAEGNN--IDPF 45

QY 61 TVKDAGTGVSVGGIILGVGVPPAGALTSFYQSFLNTIWPSDADPKMAQVEVLIDK 120
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
46 VSASTVQTGINIAGRIILGVLPFAGQLASFYSLVGEIWPGRDQWEI FLEHVEQLNQ 105

QY 121 KIBEYAKSKALAELOQNNFEDYVNALNSWKKTPLSLRSKRQDRIRE-LFSQ---AES 176
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
106 QITENARNTALARLOGLGDSFRAYQOSLEDWLE-----NRDARTSVLYTYQYIALEL 158

QY 177 HFRNSMPSFAVSKFEVLFLPTYAQAANTHLLLLKDAQVGEEGYSESDVAEYFHRQLK 236
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
159 DFLNAMPFAIRNOEYVPLLMVYQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVER 218

QY 237 TQOYTDHCYVNVYVGLNGLSYDAWKFNRRERMTLVLDLVLFPYDRLVSKGV 296
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
219 TRDYSYCVIEWNTGLNSLRGTNAASWVRYNQRRDLTLGLVDLVALFPYSYDTRTYPI 278

QY 297 KTELTRDIFTDPI-----FSLNTLQOYGPFTLSIE-NSIRKPHLPDYLOGIEFHTRLQ 348
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
279 SAQLTREVTYDAIGATGVNMAWNNVNNAPSFAIEAAAIRSPHLLDPLEQITIFS-AS 337

QY 349 PGYFGKDSFNYSNGVYETRPSIGSSKTIITSPYQ--DKSTEPVKQLSPDGQKYRTIAN 406
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
338 SRWSNTRHMYWRGHTIQSRPIGGGLTST--HGATNTSINPV-TLRFASRDVYRTESY 393

QY 407 TDVAAMPNGKYL----GVTKVDFSQYDDQK-NETSTQTYDSCRNGHVSQAQSIDQLPP 461
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
394 AGVLLM---GIYLEPIHGVTFRFNTNPQNISDRGTANYSQPYESFGLQKDSLETLP 450

QY 462 ETTDEPLEKAYSHQLNVAECFLMQDRGTIPFTTWRHSVDFNTIDA EKITQLPVVKAY 521
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
451 ETTERPNYESYSHRLSHIGILOS--RVNVPVSWTHRSADRNTIGPNRITQIPVKAS 508

QY 522 ALSGASIIPEGPGFTGNLLFLKESNSIAKFKVTLSAALLQRYRIRYASTTNLRLF 581
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
509 ELPGQTTVVRGPGFTGGDIL-RRNTGCGPIRVTVN-GPLTQRYRIGFYASTVDPDF 566

QY 582 VQNSN---NDELVIYINKTKNKKDDLTQYTFDLATNNSMGFGSGDKNELIIGAESFVNE 638
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
567 VSRGGTTVNNFRFL---RTWNSGDELKYNFVRAFTTPTFTQIQDIIRTSIQGLSGNG 623

QY 639 KIYDKIEPIPV 650
```



```
Db          624 EVYIDKIEIIPV 635
:::|||||
RESULT 28
Q93T75      PRELIMINARY; PRT; 1228 AA.
ID Q93T75
AC Q93T75;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-WAR-2004 (TREMBLrel. 26, Last annotation update)
DE Delta-endotoxin Cry1Ba2.
GN Name=cry1Ba2;
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-9;
RA Mat Isa M.N., Abdullah M.A.P., Mahadi N.M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF363025; AAKS1084.1; -.
DR HSSP; P07130; 1DLC.
DR GO; GO:0005102; P:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; Endotoxin.
DR InterPro; IPR005639; endotoxin N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin C; 1.
DR Pfam; PF00555; Endotoxin M; 1.
DR Pfam; PF03945; Endotoxin N; 1.
SQ SEQUENCE 1228 AA; 139620 MW; 3DA2A4DF59C95C3 CRC64;

Query Match 31.4%; Score 1070.5; DB 2; Length 1228;
Best Local Similarity 36.2%; Pred. No. 3.9e-61;
Matches 242; Conservative 123; Mismatches 252; Indels 51; Gaps 17;

QY 1 MNPNNRSEHDTTKVTPNSELOTHNQYPLADNPNTLEELNYKEFLRMTESSTEVLNS 60
DB 1 MTSNRKNEEIIIVANSNSAQM-----LLPDARIEDSLCIAEGNN---IDPF 45
61 TVKDAVGTSVVGQILGVGVPPFAGALTSFYQSFLNTIWPSDADPWKAFMAQVEVLIDK 120
DB 61 TVKDAVGTSVVGQILGVGVPPFAGALTSFYQSFLNTIWPSDADPWKAFMAQVEVLIDK 120
46 VSASTVQTGINAGILGVGVPPFAGALTSFYQSFLNTIWPSDADPWKAFMAQVEVLIDK 105
QY 121 KIEYAKSKALAELOGLQNPFEDYVNALNSWKKTPLSLRSKRSQDRIRFLFSQAESHFN 180
DB 106 QITENARNTALRLQGLGDSFRAYQOSLEDWLE---NRDDARTSRVLHTQYIALELDELN 162
181 SMPSPAVSKFEVLFLPTAQAAANTHLLIKDAQVGEENGYSSEDAVAFYHRLQKLTOY 240
DB 163 AMPLFAIRNQEVPLLMVYQAANLHLLRLDASLFGSEFGLTSQBIQRYERYQVTRDY 222
241 TDHCYNNVNGLGRGSGYDAWKFNRPRRMTLTLDLIVLFPFYDRLYSKGKTEL 300
DB 223 SDYCVENWTGLNSLRGTAAASWVYNQPRDLTLGVLDLVALFSDYTRTYPINTSACL 282
301 TRDIFTDPI-----FSLNTLOEQYPTFLSIE-NSIRKPHLFDYLOQIEFHRLQPGYF 352
DB 283 TREVYTDAGATGVNNAASWVYNQPRDLTLGVLDLVALFSDYTRTYPINTSACL 341
353 GKDSFNYSNGVNEVTPSPISGSKTITSPPYG--DKSTEPVQLSPDGQKVYRTIANTDVA 410
DB 342 NTRHMTYWRGHTIQSRPTGGGLNTST---HGATNTSINPV-TLRFASRDVYKTSYAGVL 397
411 AMPNGKAVYL----GVTKVDFSDYDQK-NETSTQYDSKRNNGHVSAQDSIDQLPPETTD 465
398 LW---GIVLEPHGVPTVRFNFTNQNSDRGTANYSQPYESPGQLKDSFTELPETTE 454
466 EPLEKAYSHQLNASCFLMQDRRGITPFTTHTHRSVDFNFNTDASKITQLPVPVKAYALSS 525
:::|||||
```



```
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE CryiBII.
GN Name=cryIIBII;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Isakova I.A., Isakov Y.B., Rymar' S.E., Yarovoi S.V.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY138457; AAM93496.1; -
DR HSSP; P02965; 1CIY
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR008979; Gal_bind_Like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1231 AA; 139764 MW; C9F2848A9297TEA00 CRC64;

Query Match 30.7%; Score 1053; DB 2; Length 1231;
Best Local Similarity 36.1%; Pred. No. 5.5e-60;
Matches 243; Conservative 114; Mismatches 261; Indels 56; Gaps 17;

QY 1 MNPNNRSHDTIKVTPNSELQTNHQYPLADNPSTLELANKYKFLRMTEDS---STEV 56
DB 1 MTSNRKNEEII-----NALSIPTVSPST---QMNLSPDARI-EDSLCVAEYNN 46

QY 57 LNSTVKDVGAGTGISVVGQILGVGVPPFAGALTSPYQSFINTIWPSSDADPWKAFMAQVEV 116
DB 47 IDPFVSASTVQTGINIAGRIILGVGVPPFAGALTSPYQSFINTIWPSSDADPWKAFMAQVEV 106

QY 117 LIDKKEEYAKSKALAELOGLQNNEDYVNALNSWKKTPLSLRKRSQDRIRLEFSQAES 176
DB 107 LIRQQQVTRNTATARLEGLRGVRSYQOALETMDL---NRNDARSRILIERVVALEL 163

QY 177 HFRNSMPSFAVSKFEVLFTPTAQAAANTHLLLLKDAQVFGEEGWYSSSEDVAEFYHRLQL 236
DB 164 DITTAIPLFRIRNEEVPLLMVYQAANLHLLLRDASLFGSEWGMASDVNQYQEQIRY 223

QY 237 TQYTDHCNNVNVGLNGRGSTYDAWVKNFRREMILTVDLVLFPFYDIRLYSKGV 296
DB 224 TBEYSNHCQVYNTGLNLRGTNAESWLRYNQFRDLTLGLVDLVALFPSTYDTRTPYNT 283

QY 297 KTELTRDIFTDPI-----FSLNTLOEYGTPLFSLIENSI-RKPHLPDYLGIEFHTR 346
DB 284 SAQLTRHEIYTDPIGRTNAPSGFPASTNFWNNAPFSAIEAALFRPHLLDFPEQLTIYS- 342

QY 347 LQPGYFGKDSFNWYSGVYETRPISGSKTITSPFYGDKSTEFVQKLSFDGQKVRTIAN 406
DB 343 ASSRWSSTQHMVYVGHRLNFRPIGTLNTSTQGLTNNTSINPV-TLQTSRDVYRTESN 401

QY 407 TDVAAMPNGKVLGVTKVDFPSQVD-----DQKV--FTSTQTVDSKRNNGHVSQAQSIDOL 459
DB 402 A-----GTNLFTTPVNGVPMDFRNFNPQNIYERGATTYSQPYQGVGIQLFQSETEL 454

QY 460 PPETDEPLEKAYSHOLNAEACFLMQDRGTTIPFFTWTHRSVDFNTIDAEKITQLPVVK 519
DB 455 PPETTERPNVESYSHLSHIGLIIGNTLRA--PVYSWTHRSADRTNITGNRITQIPAVK 512

QY 520 AYALSSGASIIIEGFTGGNLLFLKSSNSIAK---FKVTLNSAALLQRYVRIRYASVT 576
DB 513 GRFLFNG-SVIGSGPGFTGGDVRLNRNGNIQNRGIEVPIQSTSTSTRYVRVRYASVT 571

QY 577 NLRFLVQNSNDPLVYIYNKMKDDLLYQTFDLATTSNMFGSGDKNELIIGAESFVS 636
DB 572 SIELNVNLGNSSIFTNTLPATAASLNL--QSGDFGVYEVINNAFTSATGN-IVGARNFSA 628

QY 637 NEKIYIDKIEFIPV 650
DB 629 NAEVIIDREFEIPV 642

RESULT 32
CLIC_BACTU STANDARD; PRT; 719 AA.
AC 087404;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE pesticidal crystal protein cryIIc (Insecticidal delta-endotoxin
DE CryII(c)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
GN Name=cryIIc; Synonyms=cryII(c);
OS Bacillus thuringiensis.
OG Plasmid.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C18 / Egypt;
RA Osman Y.A., Madkour M.A., Bulla L.A. Jr.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_Like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Plasmid; Sporulation; Toxin.
SQ SEQUENCE 719 AA; 81210 MW; 8370B3F06B905DFF CRC64;

Query Match 30.7%; Score 1046.5; DB 1; Length 719;
Best Local Similarity 35.4%; Pred. No. 6.9e-60;
Matches 243; Conservative 130; Mismatches 238; Indels 75; Gaps 19;

QY 1 MNPNNRSHDTI-----KVTPESELQTNHQYPLADNPSTLELANKYKFLRMTEDSS 53
DB 1 MKLKMPDKHQTLSSNAKVDTATDS-----LKNETDIELKMNNDYLRMSEHS 50

QY 54 TEVLNSTVKDVGAGTGISVVGQILGVGVPPFAGALTSPYQSFINTIWPSSDADPWKAFMAQ 113
DB 51 ---IDPFVSASTVQTGINIAGRIILGVGVPPFAGALTSPYQSFINTIWPSSDADPWKAFMAQ 107

QY 114 VEVLIDKKEEYAKSKALAELOGLQNNEDYVNALNSWKKTPLSLRKRSQDRIRLEFSQ 173
DB 108 VEATINRKISTYARNKALTDLKGLGDALAVHESLESVWG---NRNTRARSVVKNQYIA 164

QY 174 AESHPFNMSPSFAVSKFEVLFTPTAQAAANTHLLLLKDAQVFGEEGWYSSSEDVAEFYHRLQ 233
DB 165 LELMFVKQLPSPFAVSGEEVPLLPYQAANLHLLLRDASIFPKNGGLSASEISTFYNRQ 224
```

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QY 234 LKLTQQTTHCVMYVGLNGLRSTYDAWKENFRREMTLTVDLIVLFPFPIRLYS 293
Db 225 VERTDYSYHCVKWNTGLNLRATNGQSVRYNQFRKDIELMWLDLVRVPSTLVYP 284
QY 294 KGVKTELTRIDFTPIESLNTLQ-----EYGPFTLSIENS-IRKPHLFDYLOQIEF 343
Db 285 IKTSQLTREYVTDATGVDPNQALRSTTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTI 344
QY 344 HTRLQPGYFGKDSFNYSWGNVETRRPSIGSKTITSPFYGDKST--EPVQKLSFDGOKVY 401
Db 345 YSLLS-RWSNTQYNNMGHRLSRPIGGALNTSTQ---GSTNLSINPV-TLQFTSRDFY 399
QY 402 RTIANTDVAAMPNGKVYL-----GVTKVDFSQVDDQKNETSTQYDSKRNGHVA---452
Db 400 RT-----ESWAGLNLFELTPQVNGVPRVDF-----HWKFTPLPIASDNFFYLVGAVGTQL 449
QY 453 QDSIDQLPPTTDEPLEKAYSHQLNYAECLFMQDRGTIPFTWTHRSVDFTTIDAEKI 512
Db 450 QDSENELPPTTQGPNYESYSHRLSHIG--LIGSHVKALVYSWTHRSADRTNTIEPNSI 507
QY 513 TQLPVKAYALSSGASIIIEGPGFTGNNLFLKSSNSIAKPKFTLSAALLQRYVRIRY 572
Db 508 TQPLVKAFNLSSGAAVRPGFTGGHIL-RRYKSGTFGHIRVNIN-PPFAQIRVRMSY 565
QY 573 ASTNLRLFVQ-----NSNNDFLVIYINKMKDDDLTYQTDFLATNSNMGFSGDKNE 626
Db 566 ASTDLQFHTSINGKALNQCNG-----FSATMNRGDELDTKTRTVGFTTTPFSFSDVQST 619
QY 627 LIIGASFSVNEKIYIDKIEFIPVQL 652
Db 620 FTIGAMNFSNGEYVIGRIEFVPEV 645

RESULT 33
C1BD_BACTZ
ID C1BD_BACTZ STANDARD; PRT; 1231 AA.
AC Q9ZAZ5;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIbD (Insecticidal delta-endotoxin
DE CryIb(d)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name=cryIbD; Synonyms=cryEI, cryIb(d), cryIaI;
OS Bacillus thuringiensis (subsp. wuhanensis).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=52024;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-525;
RX MEDLINE=20153386; PubMed=10688690;
RA Kuo W.-S., Lin J.-H., Tzeng C.-C., Kao S.-S., Chak K.-F.;
RT "Cloning of two new cry genes from Bacillus thuringiensis subsp.
RT wuhanensis strain,";
RL Curr. Microbiol. 40:227-232(2000).
CC -I- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut
CC epithelial cells of lepidopteran larvae. Toxic to Plutella
CC xylostella.
CC -I- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -I- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -I- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U70726; AAD10292.1; -.
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DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005639; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR Sporulation; Toxin.
DR SEQUENCE 1231 AA; 139654 MW; 129A0371CDDBEES2 CRC64;

Query Match 30.6%; Score 1042; DB 1; Length 1231;
Best Local Similarity 35.5%; Pred. No. 2.9e-59;
Matches 239; Conservative 120; Mismatches 260; Indels 54; Gaps 16;

QY 1 MNPNNSEHDTIKVTNSELQTHNNQYPLADNPNSTLE---ELNYKEFLAMTSDSSTEV 57
Db 1 MTSNRKNENBII-----NALSIPAVSNHSAQMDLSLDARIEDSLCAEIGNNINPL 50
QY 58 DNSTVKDVGTVGISVVGQILGVGVFPAGALTSTFYQSFLNTIWPSPDADPKAFMAQVEVL 117
Db 51 VSAS---TQVTGINIAGRIAGLVGVFPAGQLASFYSLVGLWPSGRDPHEIFLEHVEQL 107
QY 118 IDKKIEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSDQRIELFSQAES 177
Db 108 IRQVVTENTNTAIAARLEGGLRGVRSYQQALETWLD---NRNDARSRSIILERYVALELD 164
QY 178 FRNSMSPFAVSKEVFLPTFYAAQANTHLLLLKDAQVGEWGYSSYEDVAEFTHRQLKLT 237
Db 165 ITTAIEPLFRIRNEEVLPMVYAAQANLHLLLLDASLFGSEWGMASDVNQYQEQIRYT 224
QY 238 QQYTDHCVNMYNVLNGLRGSTYDAWKENFRREMTLTVDLIVLFPFPIRLYSKGVK 297
Db 225 EYSNHCVQWYNTGLNLRGTAESWRINQFRDLTLGVLDLVALFPSTDTTYPINTS 284
QY 298 TELTRDIFTDPI-----PSLNTLQEQYPTFLSIENSI-RKPHLFDYLOQIEPHTRL 347
Db 285 AQUTREIYTDPIGRTNAPSFGFASTNNFNNSAPSFAIEAAIFRPHLLDPPEQLTIYS-A 343
QY 348 QPGYFKDQSFNYSWGNVETRRPSIGSKTITSPFYGDKSTEPVQKLSFDGOKVYRIANT 407
Db 344 SRWSSTQHMVYVGHRLNFRPIGGTTLNTSTQGLTNTNTSINPV-TLQFTSRDYRTESNA 402
QY 408 DVAAMPNGKVYLVGTQVD-----PSQYDDQK-NETSTQYDSKRNGHVAADSIDOLP 460
Db 403 -----GTNILEFTTPVNGVPHARFNPQNIYERGATYSQYQGVGLQDSETELP 455
QY 461 PETTDEPLEKAYSHQLNYAECLFMQDRRGTPFTWTHRSVDFTTIDAEKITQLPVPVKA 520
Db 456 PETTERPNYESYSHRLSHIGLIIGNTLRA--PVYSWTHRSADRTNTIGPNRIITQIPAVKG 513
QY 521 YALSSGASIIIEGPGFTGNNLFLKSSNSIAK---FKVTLNSAALLQRYVRIRYASTTN 577
Db 514 RFLFNG-SVISGPGFTGVDVRLNRNNGNIQNRGYIEVPITQFTSTSTRYVRVRYASVTS 572
QY 578 LRLPVQNSNNDFLVIYINKMTKDDDLTYQTDFLATNSNMGFSGDKNELIIGAESFVSN 637
Db 573 IELNVLGNSSFTNTLPTAASLDNL--QSGDFGVVEINNAFTSATGN-IVGARNFSA 629
QY 638 EKIIDKIEFIPV 650
Db 630 AEVIDRPFPIPV 642

RESULT 34
C9DA_BACTP
ID C9DA_BACTP STANDARD; PRT; 1169 AA.
AC O06014;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cry9Da (Insecticidal delta-endotoxin
DE CryIXD(a)) (Crystalline entomocidal protoxin) (132 kDa crystal
```

DE	GN	Name=cry9Da; Synonyms=cryIXD(a);	Db	402	VGANINVQNDIYQIIISQVSNFASPVGSSY-SVMDTNFYLSGQVSGISGYTQGGIPAVC	460
OS	Bacillus	thuringiensis (subsp. japonensis).	Qy	443	-SKRNCHVSAQSDIDOLPPTTDEPLEKAYSHQNVASCFMLQDR-	-----GTIPP 493
OC	Bacteria;	Firmicutes; Bacillales; Bacillaceae; Bacillus.	Db	461	LQQRN-----STDELPISLNPEDGIIRNYSHRLSHITQTRFOATOGSGPSTVSANLPT	512
OX	NCBI_TaxID=128936;		Qy	494	FTWTHRSVDFENTIDAEKITQLPVVKAYALSASGASIIIEGPGFTGNGNLLFLKESNSIAKF	553
RN	SEQUENCE FROM N.A.		Db	513	CWTHRDVLDLNTITANQITQLPLVKAYELSSGATVVKGFGTGGDVI-RRTNTGGFGAI	571
RA	Asano S.;		Qy	554	KVLNSAALQRYVRIRYASTNLRLFVQNSNNDFLVIYINKTKDDDLTYTTFDLAT	613
RL	Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.		Db	572	RVSV-TGLPTQRYAIRFRYASTIDFDFVTRGGTTINNFRFTTRMNRQESRYESYRTVE	630
CC	!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut epithelial cells of insects.		Qy	614	TNSNMGSFGDKNELIIGAESFVSNEKIYIDKIEPIV	650
CC	!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.		Db	631	FTTFFNFTQSDIIRTSIQGLSGNGEVLDRIEIIPV	667
CC	!- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.					
CC	!- SIMILARITY: Belongs to the delta endotoxin family.					
CC	-----					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).					
CC	-----					
DR	EMBL; D85560; BAAL19948.1; -					
DR	HSSP; P07130; IDLC.					
DR	InterPro; IPR001178; Endotoxin.					
DR	InterPro; IPR005638; endotoxin_C.					
DR	InterPro; IPR005639; endotoxin_N.					
DR	InterPro; IPR008979; Gal_bind_like.					
DR	Pfam; PF03944; Endotoxin C; 1.					
DR	Pfam; PF00555; Endotoxin M; 1.					
DR	Pfam; PF03945; Endotoxin N; 1.					
KW	Sporulation; Toxin.					
SQ	SEQUENCE 1169 AA; 132228 MW; 659AB257229DSE59 CRC64;					
	Query Match 30.6%; Score 1041.5; DB 1; Length 1169;					
	Best Local Similarity 34.7%; Pred. No. 2.9e-59;					
	Matches 242; Conservative 121; Mismatches 257; Indels 77; Gaps 18;					
Qy	1	MNPNNRSEHDTIKV----TPNSELQTNHQNQYPLADNPSTLBEALNYKEFLRMTEDSSSTEV	56			
Db	1	MNRNNQNEYEVIDAPHCGCPADVV---KYPTDDFNAGLQNMNTKEYLYYGGDYTD	56			
Qy	57	LQNSTV---KDAVGTGISVVGQILGVGVFPAGALTSTFYQSFPLNTIPSDADP-WKAFM	111			
Db	57	LINPNLSVSGKDIQVGINIVGRLLSFFGFPFSSQWVTVYTLNLSLWPDDENSVWDAPM	116			
Qy	112	AQVEVLIDKKIEYAKSKALAELOGLQNNPFDVYNALNSWKTPTLSLRKRSQDRIRLEP	171			
Db	117	ERVEELIDQKISEAVKGRALDDLTGLQYNNVLYVEALDEWLRNPGARASLSQR----	172			
Qy	172	SQASHFRSMPSF----AVSKEVLFLPTYAQAANTHLLLLKDAOVFGREWYSSSDVA	227			
Db	173	NILDSLFTQPMPSFGSGPGSQNTATILLPVYAQANLHLLLLKDAIYGARGLNQTQID	232			
Qy	228	EYHRLQKLTQQYTDHCVWYNNVGLNGLRGSTYDAWVKFNFRREMTLTLVLDLVLFPFY	287			
Db	233	QFHSRQOSLTQTYTNHCVTAYNDGLAELRGTTAESFKYQYRREMTLTAMDVLVAFPPY	292			
Qy	288	DRLYSKGVKTELRDITFDPIFSMLNTQYGT-----FLSTENS- 328				
Db	293	NLRQYDPGTNPQLTREYITDPI-AFPLEQ--PTQLCRSWYINPAFRNLNFPVLENSL	349			
Qy	329	IRKPHLDYLOGLIEFHTRLQPGYFGKDSFNYSNGVNTETPSIGSKTTTSPYGDKSTE	388			
Db	350	IRPHLPERLUNQILVNYQ-----TNGSAWGRSV--RYHYLHSIIQEKSYGLSDP	401			
Qy	389	PVOKLSPDGQVRYRTIANTDVAAMPNGKVLYGVTKVDFSQYDQDKNETSTQTYD-----	442			
		Query Match 29.9%; Score 1018; DB 2; Length 1154;				
		Best Local Similarity 34.8%; Pred. No. 9.8e-58;				
		Matches 241; Conservative 126; Mismatches 244; Indels 82; Gaps 21;				
Qy	1	MNPNNRSEHDTIKVTPNSELQTNHQNQYPLADNPSTLBEALNYKEFLRMTEDSSSTEVLSNS	60			
Db	1	MNRNNQNEYEIIDGTCGCSDEVVKYPLTDDFNAGLQNMNTKEYLYYGGDYTGSLNP	60			
Qy	61	TV-----KDAVGTGISVVGQILGVGVFPAGALTSTFYQSFPLNTIPSDADP-WKAFMAQVE	115			
Db	61	NLSINTRDVLQGINIVGRVLGFLGVFPAGQVLTFTYTLNQLWPTNNNAWVEAFMAQTE	120			
Qy	116	VLIDKKIEYAKSKALAELOGLQNNPFDVYNALNSWKTPTLSLRKRSQDRIRLEPFSQAE	175			

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Db 121 ELIDQRISEQVWALDALTGIHDYNYEYLALEEMLERENGARANLAFQ-----PENLH 176
Qy 176 SHFNSPSP-----AVSKFEVLFLPTTAAQANLHLLKDAQVGEWGSSEDAVAFYH 231
Db 177 QLFVQSPGSGSGPGRDAVALLTVYAAQANLHLLKDAEYGARWGLNQGINLYN 236
Qy 232 RQLKLTQOYTDHCVNMYNGLRGSTYDAWKFNFRREMTLTVLDLVLPPFYDIRL 291
Db 237 AQDRTOIYNHCVATYRGLNLRGTNTSWNYHQFRREMTLMANDLVALPYNLRQ 296
Qy 292 YSKGVKTELTRDIFTDFISLNTLQEVG-----PTFLSIENS-IRKPHLFDYLOG 340
Db 297 YPGANPOLTRREIYTDVW-FNPPANQGLCRWRNNPYMTFSELENTFIRPHLFLRLNS 355
Qy 341 IEFHTRLOPCYFGKDSFNYSNGYVETRPISGSKTITSFPYGDKSTPEVKLSFDQKV 400
Db 356 LTINSHRFP--ISGNFMDYWAGH-----TLRRSYMNSA---VOEDSYGATTS 398
Qy 401 YRTIANTDVAAPNGKYLVLGTVKDFSQ-----YDQK-----NETSTQTYDSKRN 446
Db 399 TRVTINTGV---NGTNRIESTAVDFRSGLLGVYGVHRSFVPGGLFNGTI-----SPAN 449
Qy 447 NGHVSQADSIDQLP-PETTDEPLEKAYSHQLNVAECPL--MQDRRGTI-----PFFTWT 497
Db 450 AGCRNLHTRDELPLEENNGSP-----SHRLSHV-TFLSFLTDQAGSIRNSGAVPLYVWA 503
Qy 498 HRSVDPFNTIDAEKITOLPVVKAVALSSGASIIEGPGFTGNNLLFLKESNSIAKPYTL 557
Db 504 RQIDLNTTITANRIITOLPLVKAASEIAAGTVVVRGPGFTGCDIL-RTSAGTIGTIRVN 562
Qy 558 NSAALLQRYVRIRYASTTNLRLFVQNSNNDLVIYINKTNKDDDLTYOTFDLATTNSN 617
Db 563 NS-PLQRYVRIRYASTTNDFNFVIRGGTVVNFTEFPTNMSGQSRYSYVTRFESTS 621
Qy 618 MGSGDKNELIIGAESFVSN-----EKIYIDKIEPIV 650
Db 622 FNELOQDTRLTLVQSFSSGQVVDRIEIPV 654

RESULT 36
Q6PYW8
ID CIBE_BACTU PRELIMINARY; PRT; 849 AA.
AC Q6PYW8
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE CrylB type crystal protein (fragment).
OS Bacillus thuringiensis (subsp. kurstaki).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RA Li M.S., Choi J.Y., Roh J.Y., Shim H.J., Boo K.S., Je Y.H.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY50734; AAS93797.1;
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defence response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
FT NON TER 849
SQ SEQUENCE 849 AA; 95886 MW; FCB98495787CF763 CRC64;

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Query Match 29.7%; Score 1013; DB 2; Length 849;
 Best Local Similarity 34.9%; Pred. No. 1.4e-57;
 Matches 243; Conservative 123; Mismatches 226; Indels 104; Gaps 23;

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Qy 1 MNPNNSEHDTIKVTNPSELQTNHNOYPLADNPNTLE---ELNYKEFLRMTESSTEVL 57
Db 1 MTSNRKNENIIL-----NALSIPAVNSHAQNNLSTDAKIEDSLCIAEINN---I 47
Qy 58 DNSTVDKADVTGTSVVGQILGVVGVBPAGALTTSFYQSLNTIWPFSADADPWKAFMAQVEVL 117
Db 48 DPFVSASTVQTGINIAGRILGLVGVFPAGQIASFYSFLVAGELMPGRDPEIFLEHVQL 107
Qy 118 IDKKIEYAKSKALAELOGLQNNFEDYVNALNSWKKTPLSLRKSRSQDRIRE-LFSQ--- 173
Db 108 IRQQVNTTRDTALARLOGLNSFRAYQQSLEDWLE-----NRDDARTSRVLYTQYIA 160
Qy 174 AESHFNSMPSFAVSKFEVLFLPTYAQAANTHLLKDAQVGEWGSSEDAVAFYHQ 233
Db 161 LELDFLNAMPLFAIRNQEVPLLMVYAAQANLHLLKDAEYGARWGLNQGINLYN 220
Qy 234 LKLTQOYTDHCVNMYNGLRGSTYDAWKFNFRREMTLTVLDLVLPPFYDIRLS 293
Db 221 VEKTRYSYDCARWYNTGLNNLRGTNAESMLRYNQFRRLDTLGLVLDLVALFPSTYDTRVP 280
Qy 294 KGVKTELTRDIFTDPI-----PSLNTLQEVGFTFLSIENS-IRKPHLFDYLOGIEP 343
Db 281 MNTSAQLTRREIYTDPIGRTNAPSGFASTNWFNNAPSFSAIEAAVIRPPHLLDFPEQLTI 340
Qy 344 HTLQPCYFGKDSFNYSNGYVETRPISGSKTITSFPYGDKST--EPVOKLSFDGOKVY 401
Db 341 FSVLS-RWNTQYMYNTWVGHRLSRTIRGSLSTST---HGNTWTSINPV-TLQFTSRDVP 395
Qy 402 RT-----IANTDVA-----WPN-----GKV-LGVTKVDFSFQDQKNETST 438
Db 396 RTESFAGINILLTTPVNGVPWARFNWRNPLNSRLGSLTYIGTVG-----GT 443
Qy 439 QTVDSKRNNGHVSQAQSIDQLPPTTDEPLEKAYSHQLNVAECFLMQDRRGTTIPFTTWT 498
Db 444 QLFDS-----TELPETTERPNYESYHRLSNIR--LISGNTLRAPVYSWTH 489
Qy 499 RSVDFPNTIDAEKITOLPVVKAVALSSGASIIEGPGFTGNNLLFLKESNSIAKFKVTLN 558
Db 490 RSADRTNTISSDSITQIPVKSNLNSGTSVSGPGFTGDDII-RTNNGSVLSMGLNPN 548
Qy 559 SAALLQRYVRIRYASTTNLRLFVQNSNNDLVIYINKTNKDDDLTYOTFDLATTNSN 618
Db 549 NTS-LQRYVRIRYAAASQTMVLRVTVGSGTTPDQGFPTMSANESLTSQSFRFAEPPVGI 607
Qy 619 GFGDKNELIIGAESFVSN-----EKIYIDKIEPIV 650
Db 608 SASGSQT-----AGISISNNAAGRTQTFHDKIEPI 638

RESULT 37
CIBE_BACTU
ID CIBE_BACTU STANDARD; PRT; 1227 AA.
AC O85805;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein crylBe (Insecticidal delta-endotoxin)
DE CrylB(e) (Crystalline entomocidal protoxin) (139 kDa crystal protein).
OS Bacillus thuringiensis.
OG Plasmid pMVC2383.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL B-18872 / PS158C2;
RA Payne J.M., Cummings D.A., Cannon R.J.C., Narva K.E., Stelman S.;
RL "Bacillus thuringiensis genes encoding lepidopteran-active toxins.";
CC Patent number US5723758, 03-MAR-1998.
CC -!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut
CC epithelial cells of many lepidopteran larvae.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during

```

sporulation and is accumulated both as an inclusion and as part of the spore coat.

-!- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.

-!- SIMILARITY: Belongs to the delta endotoxin family.

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EMBL; AF077326; AAC32850.1; --
HSSP; P07130; IDLC.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Plasmid; Sporulation; Toxin.
SQ SEQUENCE 1227 AA; 139084 MW; CBA847BEA0B34CD3 CRC64;

Query Match 29.7%; Score 1013; DB 1; Length 1227;
Best Local Similarity 34.9%; Pred. No. 2.3e-57;
Matches 243; Conservative 123; Mismatches 226; Indels 104; Gaps 23;

QY 1 MNPNNRSEHDTIKVTPNSELOTHNNOYPLADPNSTLE---ELNYKEFLRMTEDSDSTVL 57
DB 1 MTSNRKNEVNI-----NALSIPAVNSHSAQMNLSTDAIEDSLCIAEGNN---I 47

QY 58 DNSTVKDAGTGISVVGQILGVGVPPFAGALTSFYQSFLNTTWPSDADPWKAFMAQVEVL 117
DB 48 DPFVSASTVQTGINAGTILGVLPVFPAGIASFYSFLVGLWPRGRDPWEIFLEHVEOL 107

QY 118 IDKTEEVAKSKALAELOGLQNNFEVDYVNALNSWKTPLSLRSKSQDRIRE-LFSQ--- 173
DB 108 IQQVTEVTRDTALAKLQGLGNSFRAYQQSLSDWLE-----NRDDAKTRSVLYTYQYA 160

QY 174 AESHFRNSMPSFAVSKFEVLFLETPYAAQANTHLLLLKDAQVGEWGYSSSDVAFYHRQ 233
DB 161 LELDFLNAMPLFAIRNOEVPFLMVYAAQANTHLLLLRDASLFGSEGLTSQBIQRYVERQ 220

QY 234 LKLTQQYTDHCYNNVNVGLNGLRGSTDYDAWVFNFRREMTLTVDLVLFPFYDIRLYS 293
DB 221 VEKTRSYDYCARWYNTGLNNLRGTNAESWLRYNQFRRLDTLGLVLDLVALFPSTYTRVYP 280

QY 294 KGVKTELTDRIDFTDPI-----FSLNTLQEGYPTFLSIENS-IRKPHLFDYLGQIEF 343
DB 281 MNTSAQLTREIYTDIGRINAPSGASTWFFNNAPSFSAIBAAVIRPPHLLDFPEQITI 340

QY 344 HTRLPQGVFGKDSFNWGSNNVYETRPISGSKTITSPPFYGDKST--EPVOKLSFDQKVY 401
DB 341 FGVLS-RWSNTQYNNVWVGHRELSRTIRGSLTST--HGNTNTSINPV-TLQFTSRDVP 395

QY 402 RT-----IANTDVA-----WPN-----GKVV-LGVTKVDFSQYDDQKNETST 438
DB 396 RTESFAGINILTTPVNGVFWARFWRNRPNLNRLGSLLYTIGYGV-----GT 443

QY 439 QTYDSKRNNHGVSAQSDIDQLPPTTDEPLEKAYSHQNLNABCFMLQMDRRGTIPFFTWTH 498
DB 444 QLFDSE-----TELPETTERPENYESYSHRLSNIR--LISGNLTAPVYSNTH 489

QY 499 RSVDFNTIDAKITQLPVVKAYALSSGASIIIEGFGTGGNLLFLKESNSIAKPKVTIN 558
DB 490 RSADRTNTISSDITQIFLVKSFNLNSGTSVVSGFGFTGGDII-RTNVNGSVLSMGLNFN 548

QY 559 SAALLQRYVRIRYASTTNLRFLVQNSNNDPLVIYINKMKNDDLTQTQFDLATNSNM 618
DB 549 NTS-LQRYVRIRYAAASQTMVLRVTGGSTTFDQGFPPSTMSANESLTSQSFRFAEPVGI 607

QY 619 GFSGDKNELIIGAESFVN-----EKIYIDKIEFIPV 650
DB 608 SASGSQT-----AGISISNNAAGROTGFHFDFKIEFIP 638

RESULT 38
Q9S603 PRELIMINARY; PRT; 645 AA.
ID Q9S603;
AC Q9S603;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-WAR-2004 (TREMELrel. 26, Last annotation update)
DE Delta-endotoxin (Fragment).
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=serovar japonensis type;
RX MEDLINE=99025985; PubMed=9806979;
RA Wasano N., Ohba M.;
RT "Assignment of delta-endotoxin genes of the four lepidoptera-specific Bacillus thuringiensis strains that produce spherical parasporal RT inclusions.";
RL Curr. Microbiol. 37:408-411(1998).
DR EMBL; AF042733; AAB97923.1; --
DR HSSP; P07130; IDLC.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
FT NON_TER 1 645
FT NON_TER 645 645
SQ SEQUENCE 645 AA; 72967 MW; 143E51312B890CE3 CRC64;

Query Match 29.3%; Score 999.5; DB 2; Length 645;
Best Local Similarity 34.8%; Pred. No. 7e-57;
Matches 230; Conservative 114; Mismatches 248; Indels 69; Gaps 16;

QY 26 QYPLADNPNTLEELNYKEFLRMTEDSDSTVLDNSTV----KDAVGTGISVVGQILGVVG 81
DB 11 KYPLTDDPNAGLQNNMYKEYLQTYGGDYTDLPINPLNSVSGKDVQVGINIVGRLLSPFG 70

QY 82 VPFCALTSFYQSFLNTTWPSDADP-WKAFMAQVEVLIDKIEEVAKSKALAELOGLQNN 140
DB 71 PFFSQWTVVTVYLLNSLWPPDENSVWDAMFERVEELIDQKISEAVKGRALDDLTGLQVN 130

QY 141 FEDYVNALNSWKTPLSLRSKRSQDRIRLEFSQAESHFRNSMPSF----AVSKFVFLP 196
DB 131 YNLVLEALDEWLNRPNGARASLVSR----FNILDSLTQFWPSPGSGSQNYATILLP 186

QY 197 TYAAQANTHLLLLKDAQVGEWGYSSSDVAFYHRQKLTCQYTDHCYNNVNVGLNGLR 256
DB 187 VYAAQANLHLLLLDADYIGARWGLNQTDQFHSRQQSLTQTYTNHCVTYNDGLAELR 246

QY 257 GSTYDAWVKFNRFRREMTLTVDLVLFPFYDIRLYSKGVKTELTDRIDFTDPIFSLNTLQ 316
DB 247 GTTAESEFKYQYRREMTLTAMDVLVFPYNNLQYDPGTNPQLTREYVTDPI-AFDELE 305

QY 317 EYGT-----FLSIENS-IRKPHLFDYLGQIEFHTRLQPGYFGKDSF 357
DB 306 Q--FTTQLCRSWYNAPFRNHLNFSVLNLSLRPHLFRSLNLIQLVNYQ-----ING 357

QY 358 NYWGSNVYETRPISGSKTITSPPFYGDKSTFPVKLSFDQGVKVTYNTANTDVAAPNGKV 417
DB 358 SAWRGSRV--RYHYLHSSIIQEKSYGLLSDPVGANINVQNNNDIYQIISQVSNFASPVGSS 415


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Db 402 KNIYKT-----GSLPQGVPPYQIGYVTPYIFITRAVNFVTSQSK--TSVEKYYSKDR 453
Qy 446 --NNGHVSAD--SIDOLPPTTDEPLEKAYSHOLNVAECFLMDRR---GTIPPTTWH 498
Db 454 YYSGLPEEQVTEQLPNPSIAEPBHAYSHRLCHVTTFISVNGNKYSKDLPLPSMTH 513
Qy 499 RSVDFNTIDAEKITQLPVVKAYALSSGASIEGPGFTGGNLLPLKSSNSIAKFKVTLN 558
Db 514 SSVDFNVVPTKITQLPATKY----NVSIVKEPGFIGGDI--GKNGQILKYKYNVE 567
Qy 559 SAALLQRYVRIRVASTNLRFLVQNSNDDFLVIYINKTNKDDLLYQTFDIAATNSM 618
Db 568 DVS--QKRYRFRVRYATEGELGKIDGRTVNLVYQYKTKRAPGDPITYKAFDYLFSFSPV 625
Qy 619 GFSGDKNELIIGAESFVSNE---KIYIDKIEFIPVQ 651
Db 626 KFNASSTI-----ELFLQNKTSGTFFLAGIEIIPVK 657

RESULT 42
Q45745
ID Q45745 PRELIMINARY; PRT; 1144 AA.
AC Q45745;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Delta-endotoxin (Fragment).
GN Name:cryIX gene;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94085596; PubMed=8262221; DOI=10.1016/0014-5793(93)81613-5;
RA Shevelev A.B., Svarinsky M.A., Karasin A.I., Kogan Y.N.,
RA Chestukhina G.G., Stepanov V.M.;
RT "Primary structure of the cryX**the novel Delta-endotoxin-related
RL gene from Bacillus thuringiensis ssp. galleriae.";
RN [2]
RP SEQUENCE FROM N.A.
RA Shevelev A.B., Kogan Y.N., Kuryatov M.V.;
RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; X75019; CAAS2927.1; -.
DR PIR; S39536; S39536.
DR HSP; P07130; IDLC.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
FT NON_TER
SQ SEQUENCE 1144 AA; 129398 MW; 7D28594A19C4B065 CRC64;
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Query Match 28.3%; Score 963.5; DB 2; Length 1144;
Best Local Similarity 33.3%; Pred. No. 3.6e-54;
Matches 214; Conservative 135; Mismatches 243; Indels 51; Gaps 16;

Qy 41 NYKEFLMTE--DSTEVLDSNVKDAVGTGIVGVGLVGVVPPFAGALTSFVQSFLNTI 99
Db 19 SYKDYLMSEGDYDSYINPGNVRTGLQTDIVAVVVGALGGVGGILTGFLSTLFGFL 78
Qy 100 WPS--DADPWKAFAQVEVLIDKIEEYAKSLAEQLGQNNFEDVYNALNSKKTPLSL 158
Db 79 WPNDAQWEAFTEQMEELIEQISQVVRTALDLDLTGQINYQNYLIAKWEERPNGV 138
Qy 159 RSKRSQDIRIELFSQAESFRNMPSPF----AVSKFEVLPLPTTAAANTHLLLLKDAQV 214
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Db 139 RA-----NLVLRFEILHALFVSMPSFGSGQRFQOALLVYQAANLHLLADAER 194
Qy 215 FGEWGSYSSDVAEAFYHRQLKL--TQYTDHCNVNYNVGLNGLRGSTYDVAWVKFRFRREM 273
Db 195 YGARWGLRESQIGNLYFNEQLQTRDYTNHCNVNAYNGLAGLGRGTSAESMLKYHQFRREA 254
Qy 274 TLAVLDLVLVFPFVDRLYSKGVKTELTRDIFDTP-----IFSLNTLOEYGP 320
Db 255 TLMAMDIALFPYNTYRPIAVNPQLTRVYDPLGVPSSESLFRELCLRWQETSAM 314
Qy 321 TFLSIENS-IRKPHLFYLOGIEFHTRLOQYFGKGSFNWGSNGYVETRESIGSSKTIIS 379
Db 315 TFSLENALIISSPHLFTINNLMYTGSPSVHLTNQLIEGWHSVTSLLASGPTTVLR 374
Qy 380 PFYGDKSTEPVQKLSFDGQKYYR--TIANTDVAWPNKGYLVGVTKVDFSOYDQDKNETS 437
Db 375 RNYG-STTSIVNYSFNDRDYYQINRSHSTGL-GFQNAPLF-GITRAQF-----YP 422
Qy 438 TOTYDSKRNGHVSQO--DSIDOLPPTTDEPLEKAYSHOLNVAECFL-----MODR 487
Db 423 GGTYSVTQNALTCQYNYSIDELPSLDNPEISRSYSRHSHTSILHRLVITDGINY 482
Qy 488 RGTIPPTTTHRSVDFNTIDAETITQLPVVKAYALSSGASIEGPGFTGGNLLFLKSS 547
Db 483 SGNLPTVWTHRDVLDNTITADRIITQLPLVKSFEIPAGTTVVRGPGFTGGDIL-RTGV 541
Qy 548 NSIAKPKVTLNSAALLQRYVRIRYASTNLRFLVQNSNDDFLVIYINKTNKDDLLTYQ 607
Db 542 GTEGTIRVR--TTAPLTQRYRIRFRFASTNLFTGIRVGDRQVNYFDFRGTMRGRDELYE 600
Qy 608 TFDLATNNSMGFGDKNELIIGAESFVSNEKIYIDKIEFIPV 650
Db 601 SFATREFTDFFRQFQELISVFANAFSAGQEVFDRIEIIPV 643

RESULT 43
C1CA_BACTE STANDARD; PRT; 1189 AA.
AC P05518; P10327; Q03742; Q45725;
DT 01-NOV-1988 (Rel. 09, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIcA (Insecticidal delta-endotoxin
DE CryIC(a)) (crystalline entomocidal protoxin) (134 kDa crystal protein).
GN Name:cryIcA; Synonyms=cryIC, cryIC(a);
OS Bacillus thuringiensis (subsp. entomocidus), and
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1436, 1433;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.entomocidus; STRAIN=60.5;
RX MEDLINE=88289380; PubMed=3399402;
RA Honee G., van der Salm T.P.M., Visser B.;
RT "Nucleotide sequence of crystal protein gene isolated from B.
RT thuringiensis subspecies entomocidus 60.5 coding for a toxin highly
RT active against Spodoptera species.";
RL Nucleic Acids Res. 16:6240-6240(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.aizawai; STRAIN=NRRL B-18484 / PS811;
RA Payne J.M. Sick A.J.;
RT "Bacillus thuringiensis isolate active against lepidopteran pests, and
RT genes encoding novel lepidopteran-active toxins.";
RL Patent number US5246852, 21-SEP-1993.
RN [3]
RP SEQUENCE OF 1-823 FROM N.A.
RC SPECIES=B.t.aizawai; STRAIN=7-29;
RX MEDLINE=89343627; PubMed=2548060;
RA Sanchis V., Lerechus D., Menou M., Chaufaux J., Guo S., Lecadet M.-M.;
RT "Nucleotide sequence and analysis of the N-terminal coding region of
RT the Spodoptera-active delta-endotoxin gene of Bacillus thuringiensis
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RT aizawai 7.29.";
RL Mol. Microbiol. 3:229-238(1989).
RN [4].
RP SEQUENCE OF 1-756 FROM N.A.
RC SPECIES=B.t.aizawai; STRAIN=7-29 / K26-21;
RA Strizhov N.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC !- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of many lepidopteran larvae including Spodoptera
CC species.
CC !- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC !- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC !- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; X07518; CAA30396.1; -
DR EMBL; M73251; AAA22343.1; -
DR EMBL; X13620; CAA31951.1; -
DR EMBL; X96682; CAA65457.1; -
DR FIR; S00944; S00944.
DR FIR; S04181; S04181.
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_Like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
FT CONFLICT 124 124 A -> E (in Ref. 1).
FT CONFLICT 294 294 A -> R (in Ref. 1).
FT CONFLICT 366 366 N -> I (in Ref. 3).
FT CONFLICT 376 380 WPAPP -> CORRH (in Ref. 3).
FT CONFLICT 386 386 T -> G (in Ref. 3).
FT CONFLICT 405 405 T -> Q (in Ref. 2).
FT CONFLICT 453 453 H -> D (in Ref. 1).
FT CONFLICT 775 775 R -> A (in Ref. 3).
FT CONFLICT 853 853 V -> L (in Ref. 2).
FT CONFLICT 864 864 G -> N (in Ref. 2).
FT CONFLICT 931 931 D -> N (in Ref. 2).
SQ SEQUENCE 1189 AA; 134715 MW; 36276B685916A0DF CRC64;

Query Match 27.4%; Score 934.5; DB 1; Length 1189;
Best Local Similarity 36.3%; Pred. No. 3e-52;
Matches 242; Conservative 103; Mismatches 227; Indels 95; Gaps 27;

Qy 21 QTNHQ---YPLADNPNTLEELNYKEFLRWTESDSTEVLDN---STVKDVGTSVVG 74
Db 3 ENNQNCIPYCNLSNPEVL-----LDGERISTGNSSIDISLSLV- 42
Qy 75 QILGVGVPPAGALTSTFYQSLNTWPSDADPKAFMAQVEVLIDKKIEYAKSKALAE 134
Db 43 QFLVSNFVPGGFLVGLIDFWGVLVGPQ---WDAFLVQEQLINEIAEFARNAIANL 99
Qy 135 QGLQNNFEDYVNALNSKKTPLSLRKSRQDRIRLELFSQAESHFRNMPFSAVKFEVL 194
Db 100 EGLNNFNIVYAEKFEEDP---NNPATRTVIDRFRILDGLERIDIPSRISGFEVPL 156
Qy 195 LPTTAQAAHTHLLLLKDAQVFGEGWYSSSEDAFFVHRLKLTQOYTHCVNMYNGLNG 254
Db 157 LSVYAQAANHLAILRDSVIFGERWGLTTINNVENNRLRHIDEYADHCANTYNRGLNW 216

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Qy 255 LRGSTYDAVKENRFRREMTLTVLDLILVLPFPYDIRLSKGVKTELTRDIFTDPIPSLN- 313
Db 217 LPKSTYQDWITYNRLRRDLTLVIDIAAFPNVDNRRYPIQPUGQLTRVYTDPLINFP 276
Qy 314 TLQEYG--PTFLSIENS-IRKPHLPDYLOGIEFHTRLPQGYFGKDSFNWGSNYVETRPS 370
Db 277 QLQSVACLPTFNWMESSAIRNPHLPDLANNLTIFT---DMFSVGRNFWYGGHRVIS--S 330
Qy 371 IGSKVIITSPFYG-DKSTEPVQKLSFDQKQVYETIANTDV---AAWPNKVVYL-GVTKV 424
Db 331 LIGGNNITSPIYGREANQEPFRSFTNG-PVFRTLSNPTLRLQLQWPAPPPFNLRGVEGV 389
Qy 425 DFSQYDDQKNETSTQTYDSKRNGHVSQAQSIDQLPPETDDEPLEKAYSHQLNVAECFLM 484
Db 390 EFS-----TPTNSFTY---RGRGTV---DSLTELPPEDNSVPPREGYSRLCHA---TF 434
Qy 485 QDRRGITPFF-----FWTHRSVDFNNTIDAEKITQLPVVKAYALSSGASIIISGPGFTGG 538
Db 435 VQRSGT-PFLTGTGVFSTHRSATLTNTIDPERINQIPLVKFRVMGTSVITGPGFTGG 493
Qy 539 NLLFLKSSNSIAKFKYTLNSAALLQRYRVRIRVASTTNLRLFV-----QNSNN 587
Db 494 DIL--RRNTFGDFVSLQVNIINS-PITQRYRLRFRIASSRDARVIVLTGAATGCGGVSVN 551
Qy 588 DFLVIYINKTKMKDDDLTYQTDFLATNSNMGFS-----GDKNELIIGAESFVSNKIKY 641
Db 552 ----MPLQKTMEIGENLTSTRFTYDFSNPFPFRANPDIIIGISQPLFGAGS-ISSGELY 606
Qy 642 IDKIEFI 648
Db 607 IDKIEII 613

RESULT 44
QSYNB8
ID Q6YNB8 PRELIMINARY; PRT; 1189 AA.
AC Q6YNB8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Delta-endotoxin (Insecticidal protein Cry1Ca).
GN Name=cry1C; Synonyms=cry1Ca;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1].
RP SEQUENCE FROM N.A. PubMed=14629010;
RX MEDLINE=22990512; Tseng C.C., Tsai Y.S.;
RA Kao S.S., Hsieh F.C.;
RT "Cloning and expression of the insecticidal crystal protein gene
RT Cry1Ca9 of Bacillus thuringiensis G10-01A from Taiwan granaries.";
RL Curr. Microbiol. 47:295-299(2003).
RN [2].
RP SEQUENCE FROM N.A.
RA Kao S.-S., Hsieh F.-C.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [3].
RP SEQUENCE FROM N.A.
RC STRAIN=c002;
RA Chen Z., Wu X., Zhang J., Yao J., Huang D.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY078160; AAL79362.1; -.
DR EMBL; AF362020; AAM00264.1; -.
DR GO; GO:0005102; P.receptor binding; IEA.
DR GO; GO:0006952; P.defense response; IEA.
DR GO; GO:0003405; P.pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.

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SQ SEQUENCE 1189 AA; 134714 MW; 362768685916A0DF CRC64;
Query Match 27.4%; Score 934.5; DB 2; Length 1189;
Best Local Similarity 36.3%; Pred. No. 3e-52;
Matches 242; Conservative 103; Mismatches 227; Indels 95; Gaps 27;

Qy 21 QTNHQ---YPLADNPSTLEELNKEFLRMTEDSSTEVLN---STVKDAVGTGISVVG 74
Db 3 ENNQNCIPYNCLSNPEVL-----LDGERISTGSSIDISLVL- 42
Qy 75 QILGVGVVPAGALTSPYQSFLNTIWPSSDADPWKAPMAQVEVLIDKKIEYAKSKALAE 134
Db 43 QFLVSNFVPGGGFLVGLIDFVWGIVGPSQ---WDAFLVQIEQLINERIAEFARNAAT 99
Qy 135 QGLONNFEDYVNALNSWKKTPLSRSKRSDRIELFSQAESHFRNSMPSFAVSKPEVL 194
Db 100 EGLGNFNIVYEAKEWEDP---NNPATRTRVIDRFRILDGLLERDIPFRISGFEVPL 156
Qy 195 LPTYAAQANTHLLLLKDAQVGEWGSSEDAEFYHRQLKLTQOYTDHCNNVYVGLNG 254
Db 157 LSVYAQAANLHLAIRDVSIFGERWGLTINNVNENRILRHIDEYADHCANTYNRGLN 216
Qy 255 LRSTYDAWVKFRPREMTLTVLDLIVLPFPFYDIRLYSGVKTELTRDITPDIFSLN- 313
Db 217 LPKSTYQDMITYNRLRDLTLVLDIAAFPNYDNRRIPIQPVGQLTREYITDPLINF 276
Qy 314 TLOEYG--PTFLSIENS-IRKPHLFDYLOGIEPHTRLQPGVFGKDSFNYSWGNVETRPS 370
Db 277 QLASVAQLPTFNWESSAIRNPHLFDILNLTFT----DWFSVGRNFYGGHRVIS--S 330
Qy 371 IGSKTITSPFYG-DKSTEPVQKLSFDGQKRYRTIANTDV---AAMPNGKVYL-GYTKV 424
Db 331 LIGGNITSPYIGREANQPPRSFTNG-PVFRTLNPTLRLQLQPPWAPPFNLRGVEGV 389
Qy 425 DFSQYDDQKNETSTQYDSCRNGHVSQAQSDIQLPPTTDEPLEKAYSHQLYAECLM 484
Db 390 EFS-----TPTNSFTY---RGRGTV---DSLTELPPEDNSVPPREGYSHRLCHA---TF 434
Qy 485 QDRRGTIPTF-----FTWTHRSVDFNTIDAETITOLPVVKAYALSSGASIIEGPGFTGG 538
Db 435 VQRSGT-PFLTGTGVFVSWTHRSATLTNTIDPERINQIPLVKGFVWGGSVITGPGFTGG 493
Qy 539 NLLFKESSNSIAKFKVTLNSAALLQRYRIRYASTTNLRLFV-----QNSNN 587
Db 494 DIL-RRNTFGDFVSLQVINS-PITQRYLRFRYASSRDARVILTGAASTGVGGQVSVN 551
Qy 588 DFLVIYINKTMKDDDLTYQTFDLATNSNGFS-----GDKNELIIGAESFVSNKIIY 641
Db 552 ----MPLQKTMIEGENLTSTRFT--RYTDFSNPFSFRANPDIIIGSEQPLFGAGS-ISSGELY 606
Qy 642 IDKIEFI 648
Db 607 IDKIEII 613

RESULT 45
Q9L877 PRELIMINARY; PRT; 1189 AA.
AC Q9L877;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Toxin CrylCa6.
GN Names-crylCa6;
OC Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A2-F;
RA Yu J., Pang Y., Li J.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF215647; AAF37224.1; -.
```


RC SPECIES=B.t.aizawai; STRAIN=HD-133;
 RA Chak K.-F., Jen J.C.;
 RT "Complete nucleotide sequence and identification of a putative
 promoter region for the expression in *Escherichia coli* of the cryIA(b)
 gene from *Bacillus thuringiensis* var. aizawai HD133.";
 RL Proc. Natl. Sci. Coun. Repub. China, B, Life Sci. 17:7-14 (1993).
 [9]
 RN SEQUENCE FROM N.A.
 RC SPECIES=B.t.aizawai; STRAIN=IPL7;
 RX MEDLINE=87248103; PubMed=3297927; DOI=10.1016/0378-1119(87)90098-9;
 RA Oeda K., Osile K., Shimizu M., Nakamura K., Yamamoto H., Nakayama I.,
 RA Ohkawa H.;
 RT "Nucleotide sequence of the insecticidal protein gene of *Bacillus*
 thuringiensis strain aizawai IPL7 and its high-level expression in
Escherichia coli.";
 RL Gene 53:113-119 (1987).
 [10]
 RN SEQUENCE FROM N.A.
 RC SPECIES=B.t.aizawai; STRAIN=IC1;
 RX MEDLINE=89083518; PubMed=3205732;
 RA Haider M.Z., Ellar D.J.;
 RT "Nucleotide sequence of a *Bacillus thuringiensis* aizawai IC1
 entomocidal crystal protein gene.";
 RL Nucleic Acids Res. 16:10927-10927 (1988).
 CC -I- FUNCTION: Promotes colloidotomic lysis by binding to the midgut
 epithelial cells of many lepidopteran larvae.
 CC -I- DEVELOPMENTAL STAGE: The crystal protein is produced during
 sporulation and is accumulated both as an inclusion and as part of
 the spore coat.
 CC -I- BIOTECHNOLOGY: Introduced by genetic manipulation and expressed in
 insect-resistant maize by Monsanto, Northrup King and Ciba Geigy.
 CC -I- MISCELLANEOUS: Toxic segment of the protein is located in the N-
 terminus.
 CC -I- SIMILARITY: Belongs to the delta endotoxin family.
 CC
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 CC
 DR EMBL; M15271; AAA22561.1; -
 DR EMBL; M13898; AAA22330.1; -
 DR EMBL; M37263; AAA22420.1; -
 DR EMBL; M12661; AAA22613.1; -
 DR EMBL; AF059670; AAC64003.1; -
 DR EMBL; D00117; BAA00071.1; -
 DR EMBL; X04698; CAA28405.1; -
 DR EMBL; X54939; CAA38701.1; -
 DR EMBL; A09398; CAA00840.1; -
 DR EMBL; A03793; CAA00303.1; -
 DR EMBL; M16463; AAA22551.1; -
 DR EMBL; X13233; CAA31620.1; -
 DR PIR; A26513; A26513.
 DR PIR; A29838; A29838.
 DR PIR; A90025; J00002.
 DR PIR; I39838; I39838.
 DR PIR; S02134; S02134.
 DR HSSP; P02965; 1CIY.
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005638; endotoxin.C.
 DR InterPro; IPR005639; endotoxin.N.
 DR InterPro; IPR008979; Gal_bind_Like.
 DR Pfam; PF03944; Endotoxin_C; 1.
 DR Pfam; PF00555; Endotoxin_M; 1.
 DR Pfam; PF03945; Endotoxin_N; 1.
 KW Genetically modified food; Plasmid; Sporulation; Toxin.
 FT CONFLICT 207 207 A -> R (in Ref. 4).
 FT CONFLICT 282 283 GS -> AL (in Ref. 9).
 FT CONFLICT 382 406 VLDGTEFAYGTSSNLPSAVYRSGT -> GPDGGRICLWNL
 LKFGPPYTEKAP (in Ref. 4).

FT CONFLICT 410 410 L -> P (in Ref. 4).
 FT CONFLICT 432 432 LSH -> CLAY (in Ref. 4).
 FT CONFLICT 437 437 R -> Y (in Ref. 4).
 FT CONFLICT 447 447 I -> V (in Ref. 4).
 FT CONFLICT 450 450 A -> P (in Ref. 10).
 FT CONFLICT 452 458 MFSWIHR -> NDSSWTYC (in Ref. 4).
 FT CONFLICT 461 461 E -> N (in Ref. 3).
 FT CONFLICT 463 465 NNI -> GDV (in Ref. 4).
 FT CONFLICT 479 486 STNLGSGT -> LOSLWN (in Ref. 4).
 FT CONFLICT 492 492 P -> L (in Ref. 4).
 FT CONFLICT 501 505 RTSP -> EELT (in Ref. 4).
 FT CONFLICT 537 537 F -> L (in Ref. 10).
 FT CONFLICT 542 542 D -> H (in Ref. 3).
 FT CONFLICT 545 545 P -> I (in Ref. 10).
 FT CONFLICT 568 568 T -> I (in Ref. 10).
 FT CONFLICT 569 569 TV -> HL (in Ref. 3).
 FT CONFLICT 665 665 K -> E (in Ref. 3).
 FT CONFLICT 675 676 KR -> NG (in Ref. 3).
 FT CONFLICT 703 703 S -> N (in Ref. 4).
 FT CONFLICT 712 712 D -> H (in Ref. 4).
 FT CONFLICT 731 731 P -> L (in Ref. 7 and 10).
 FT CONFLICT 785 785 P -> R (in Ref. 3).
 FT CONFLICT 836 836 N -> I (in Ref. 3).
 FT CONFLICT 978 978 H -> Q (in Ref. 9).
 FT CONFLICT 1016 1016 E -> T (in Ref. 3).
 FT CONFLICT 1036 1036 C -> F (in Ref. 9).
 FT CONFLICT 1060 1060 E -> G (in Ref. 3).
 SQ SEQUENCE 1155 AA; 130623 MW; 43461A64C7AC7CAF CRC64;
 Query Match 26.4%; Score 899.5; DB 1; Length 1155;
 Best Local Similarity 33.3%; Pred. No. 5.6e-50;
 Matches 220; Conservative 118; Mismatches 231; Indels 91; Gaps 24;
 QY 31 DNPSTLEELNYKEFLRMTEDESDTEVLNDSTVKDVGTSISVVG-----QILGVGVGVP 84
 DB 3 NNPNTN-ECIPY-----NCLSNPEVEVLGGERIE---TGYTIDISLSTQFLSLSEFPVG 53
 QY 85 AGALTSFYQSFLNTIW---PSDADPWKAPMAQVEVLIDKKEIYAKSKALAEQLQNN 140
 DB 54 AG-----FVLGLVDILWIGFPGSQ---WDAPLQVIEQLINQRIEFPARNQAIISLEGSLN 106
 QY 141 FEDYNALMSKKTPSLRSKRSQDRIRSELFQAEHSFRNSMPSFAVSKPEVLFLPTAYQ 200
 DB 107 YQIYAESFREWEADPTN-PALREEMRIQ--FNDMSALTAIPLFAVQNYQVPLLSVYVQ 163
 QY 201 AANTHLLLLKDAQFCEEWGYSSEDAEFYHQLKLTQYTDHCYNNVYVNLGLRGSTY 260
 DB 164 AANLHLSVLRDVSVFGQRGWFDAAATNSRYNDLTRIGNYTDHAVRYNTGLSRVWGPDS 223
 QY 261 DAWKFNRRREMTLTVLDLIVLFPFYDIRLSYKGVKTELTRDIFTDPIFSLNTLOEYGP 320
 DB 224 RDIWRYNQFRRELTTLVDIVSLFPNYDSRTYPIRTVSQLTREIYNPV-----LENFDG 278
 QY 321 TF-----LSIENSIRKPHLFDYLOGIEFHTRLOQGYFGKDSFNWNGYVETREPSIGSSKT 376
 DB 279 SFRGSAQIGEGSIRSHPLMDILNSITITVDARGEY-----YWSGHQIMASPVGSGPE 332
 QY 377 ITSPFYGDK-STEPVQKLSFD-GQKYRTIANTDVAWPNKVY-----LGVTKVDFSQY 429
 DB 333 FTTPPLYGTWGNAAPOQRIVAQLGGQYVRLSSP-----LYRRPFNIGINNQLSVL 383
 QY 430 DDQKNETSTQT-----YDSKRNNGHVSQAQDSIDLQPPETTDDEPLEKAYSHQLNYAECLF 483
 DB 384 DGEFAYGTSSNLPSAVY---RKSQTV---DSLDEIPQNNVPPQGSRLSHLSHSMFR 437
 QY 484 MQDRRTI-----PPFTWTHRSVDFNTIDAETIKQLPVVKAYALSSGASIIIEGPGFTGG 538
 DB 438 SGFSNSSSVSIIRAPMFSWIHRSAAEFNNIIPSSQITQILTKSTNLGSGTSVVKGPFTGG 497
 QY 539 NLLFLKESNSNAKPKYTLNSAALLQRYVRIRYASTTNLRLFVQ-----NSNDFLVI 592
 DB 498 DIL-RTSPGQISTURVNI-TAPLSQRYVRIRYASTTNLRPFHTS:IDGRPINQGN----- 550

Query Match	26.4%	Score 898.5	DB 2	Length 1156
Best Local Similarity	33.3%	Pred. No. 6.5e-50		
Matches	220	Conservative 118	Mismatches 231	Indels 91
Gaps	24			
QY	31	DNPNSTLEELNYKEFLRTWSDSSFEVLNDSNVKDAVGTGISVVG-----QILGVVGVPF	84	
Db	3	NNPNIN-ECIPY-----NCLSNPEVEVLGGERIE---TGYTPIDISLSTQFLISEFVPG	53	
QY	85	AGALTSFYQSFLANIW----PSDADPWFKAQVQEVLIDKKIEBYAKSKALAAELQGLQNN	140	
Db	54	AG----FVLGLVDIIWGIQFQPSQ---WDAFLVQIEQLINQRIEFARQAIISRLEGLSNL	106	
QY	141	FEDYVNALNSWKKTPLSLRKSQDRIRELPSQAEHSFRNSMPSFAVSKFEVLFLPTVAQ	200	
Db	107	YQIYAESFREWEADPTN-PALREEMRIQ---FNDMNSALTTTAIPLFVQNVQVPLLSVVXQ	163	
QY	201	AAMTHILLLLDQAQVFGGEWGYSSDDVAEFYHRQLKLTQQYTDCVNMVNGLNGRSTY	260	
Db	164	AANLHLFVLDRDVSFGQGWGFDAATINRSYNDLTRLIGNYTDHVRWYNTGLERVWGPD	223	
QY	261	DAWVKFNRFRREMTLVLDLIVLFPFFYDRIRLYSKGVKTELTRDIFTDPFPSLNTLQEXGP	320	

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